

From: Myers, Carla  
Sent: Tuesday, November 14, 2006 7:29 AM  
To: STIC-Biotech/ChemLib  
Subject: sequence search for 10/823197

Please search:

- 1) SEQ ID NO: 7
- 2) please perform a score over length search of SEQ ID NO: 7, with a minimum length of 8 nucleotides and a maximum length of 50 nucleotides, and a score over length cutoff of 70%.

Please provide an alignment in SCORE of the first 50 results (there is no need to provide a printed version of the results).

Thank you-

Carla Myers  
AU 1634  
Remsen Bldg / Rm 2E79  
Mailbox: REM 2C70  
571-272-0747

\*\*\*\*\*  
Searcher: \_\_\_\_\_  
Searcher Phone: \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date completed: \_\_\_\_\_  
Searcher Prep Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*  
Type of Search  
NA# \_\_\_\_\_ AA# \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure #: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*  
Vendors and cost where applicable  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIS: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (Specify): \_\_\_\_\_

Date completed: \_\_\_\_\_  
Searcher: Beverly e 2528  
Terminal time: \_\_\_\_\_  
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Number of Searches: \_\_\_\_\_  
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Search Site  
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\_\_\_\_ CM-1  
\_\_\_\_ Pre-S  
Type of Search  
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\_\_\_\_ A.A. Sequence  
\_\_\_\_ Structure  
\_\_\_\_ Bibliographic

Vendors  
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\_\_\_\_ Dialog  
\_\_\_\_ APS  
\_\_\_\_ Geninfo  
\_\_\_\_ SDC  
\_\_\_\_ DARC/Questel  
\_\_\_\_ Other CGN

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 21, 2006, 14:27:35 ; Search time 0.001 Seconds  
(without alignment)  
60.656 Million cell updates/sec

Title: US-10-823-197-7

Perfect score: 17

Sequence: 1 CTCAGCAACTCCTAT 17

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 0.5

Searched: 156 seqs, 1784 residues

Total number of hits satisfying chosen parameters: 312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 156 summaries

Database : rgedb:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17	100.0	17	1	ACCESSION: A82477
2	17	100.0	17	1	ACCESSION: A84740
3	17	100.0	17	1	ACCESSION: A84740
4	17	100.0	17	1	ACCESSION: BD070852
5	17	100.0	17	1	ACCESSION: BD085841
6	17	100.0	17	1	ACCESSION: BD124538
7	17	100.0	17	1	ACCESSION: BD246771
8	17	100.0	17	1	ACCESSION: BD271249
9	17	100.0	17	1	ACCESSION: CQ918145
10	17	100.0	17	1	ACCESSION: CS231184
11	17	100.0	17	1	ACCESSION: AR282877
12	17	100.0	17	1	ACCESSION: I85578
13	17	100.0	17	1	ACCESSION: AR487085
14	17	100.0	17	1	ACCESSION: AR490513
15	17	100.0	17	1	ACCESSION: AR493814
16	17	100.0	17	1	ACCESSION: AR532946
17	17	100.0	17	1	ACCESSION: AR534188
18	17	100.0	17	1	ACCESSION: AR542777
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20	17	100.0	17	1	ACCESSION: AX052797
21	17	100.0	17	1	ACCESSION: AX067286
22	17	100.0	17	1	ACCESSION: AX360017
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Myers, C  
10/823/197  
Seq: ID 7

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## ALIGNMENTS

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LOCUS Sequence 15 from Patent WO9854359.
DEFINITION A82477
ACCESSION A82477
VERSION A82477.1 GI:6732221
KEYWORDS
SOURCE unidentified
ORGANISM unclassified sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Duff,G. and Cox,A.
TITLE PREDICTION OF INFLAMMATORY DISEASE ASSOCIATED WITH IL-1 GENELOC
JOURNAL POLYMORPHISMS
PATENT: WO 9854359-A 15 03-DEC-1998;
DUFF GORDON (GB); COX ANGELA (GB)
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LOCUS Sequence 1 from Patent WO9844150.
DEFINITION A84740
ACCESSION A84740
VERSION A84740.1 GI:6733608
KEYWORDS
SOURCE unidentified
ORGANISM unclassified sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Spector,T.D. and Keen,R.W.
TITLE POLYMORPHISMS OF AN IL-1 RECEPTOR ANTAGONIST GENE
JOURNAL Patent: WO 9844150-A 1 08-OCT-1998;
GEMINI RESEARCH LTD (GB); SPECTOR TIMOTHY DAVID (GB)
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LOCUS Sequence 1 from patent US 6210877.
DEFINITION AR144074
ACCESSION AR144074
VERSION AR144074.1 GI:15105941
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Francis,S.E.; Crossman,D.C. and Duff,G.W.
TITLE Prediction of coronary artery disease
JOURNAL Patent: US 6210877-A 1 03-APR-2001;
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DEFINITION Prediction of coronary artery disease.
ACCESSION  BD070852
VERSION    BD070852.1 GI:22616455
KEYWORDS   JP 2001514522-A/1.
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
REFERENCE  1 (bases 1 to 17)
AUTHORS    Francis,S.E., Crossman,D.C. and Duff,G.W.
TITLE      Prediction of coronary artery disease
JOURNAL    Patent: JP 2001514522-A 1 11-SEP-2001;
           INTERLEUKIN GENETICS INC
COMMENT    OS Artificial Sequence
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           PI SHEILA E FRANCIS,DAVID C CROSSMAN,GORDON W DUFF PC
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DEFINITION Methods of diagnosing and treating chronic obstructive airway
ACCESSION  BD085841
VERSION    BD085841.1 GI:22631451
KEYWORDS   JP 2001522586-A/5.
SOURCE     unidentified
ORGANISM   unclassified sequences.
REFERENCE  1 (bases 1 to 17)
AUTHORS    Duff,G.W., Giovain,M., Barnes,P.J. and Rim,S.
TITLE      Methods of diagnosing and treating chronic obstructive airway
JOURNAL    Patent: JP 2001522586-A 5 20-NOV-2001;
           INTERLEUKIN GENETICS INC
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           PN JP 2001522586-A/5
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           PR 07-NOV-1997 GB 9723553.5,12-JAN-1998 US 09/005923 PI
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ACCESSION  BD124538
VERSION    BD124538.1 GI:23219483
KEYWORDS   JP 2002500513-A/15.
SOURCE     unidentified
ORGANISM   unclassified sequences.
REFERENCE  1 (bases 1 to 17)
AUTHORS    Duff,G., Cox,A., Camp,N.J. and Giovine,F.S.D.
TITLE      Prediction of inflammatory disease associated with IL-1 gene loci
JOURNAL    Patent: JP 2002500513-A 15 08-JAN-2002;
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           PD 08-JAN-2002
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           PR 29-MAY-1997 GB 9711040.7
           PI GORDON DUFF,ANGELA COX,NICOLA JANE CAMP,FRANCESCO SAVERIO DE
           PI GIOVINE
           PC C12Q1/68
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DEFINITION Diagnostics and therapeutics for sepsis.
ACCESSION  BD246771
VERSION    BD246771.1 GI:33056541
KEYWORDS   JP 2002533096-A/1.
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
REFERENCE  1 (bases 1 to 17)
AUTHORS    Giovine,F.S.D. and Duff,G.W.
TITLE      Diagnostics and therapeutics for sepsis
JOURNAL    Patent: JP 2002533096-A 1 08-OCT-2002;

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 ACCESSION BD124538  
 VERSION BD124538.1 GI:23219483  
 KEYWORDS JP 2002500513-A/15.  
 SOURCE unidentified  
 ORGANISM unclassified sequences.

REFERENCE 1 (bases 1 to 17)  
 AUTHORS Duff,G., Cox,A., Camp,N.J. and Giovine,F.S.D.  
 TITLE Prediction of inflammatory disease associated with IL-1 gene loci  
 JOURNAL Patent: JP 2002500513-A 15 08-JAN-2002;  
 COMMENT OS Unidentified  
 PN JP 2002500513-A/15  
 PD 08-JAN-2002  
 PF 21-MAY-1998 JP 1999500358  
 PR 29-MAY-1997 GB 9711040.7  
 PI GORDON DUFF,ANGELA COX,NICOLA JANE CAMP,FRANCESCO SAVERIO DE  
 PI GIOVINE  
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 CC Topology: Linear;  
 CC Prediction of inflammatory disease associated with IL-1 CC  
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RESULT 7  
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 KEYWORDS JP 2002533096-A/1.  
 SOURCE synthetic construct  
 ORGANISM other sequences; artificial sequences.

REFERENCE 1 (bases 1 to 17)  
 AUTHORS Giovine,F.S.D. and Duff,G.W.  
 TITLE Diagnostics and therapeutics for sepsis  
 JOURNAL Patent: JP 2002533096-A 1 08-OCT-2002;

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INTERLEUKIN GENETICS INC
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PR 30-OCT-1998 US 09/183850
PI FRANCESCO S DI GIOVINE, GORDON W DUFF
PC C12N15/09, A61K38/00, A61K45/00, A61P31/00, C12Q1/68, C12N15/00, PC
A61K37/02
CC Description of Artificial Sequence: primer
FH Key Location/Qualifiers
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FT /organism='Artificial Sequence'
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Best Local Similarity 100.0%; Pred. No. 8;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTCAGCAACACTCCTAT 17
Db 1 CTCAGCAACACTCCTAT 17

RESULT 8
BD271249
LOCUS BD271249 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Prediction of risk of interstitial lung disease.
ACCESSION BD271249
VERSION BD271249.1 GI:33081017
KEYWORDS JP 2002540801-A/21.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 17)
AUTHORS Duff, G.W., Giovine, F.S.D. and Whyte, M.
TITLE Prediction of risk of interstitial lung disease
JOURNAL Patent: JP 2002540801-A 21 03-DEC-2002;
INTERLEUKIN GENETICS INC
COMMENT OS Artificial Sequence
PN JP 2002540801-A/21
PD 03-DEC-2002
PF 31-MAR-2000 JP 2000609606
PR 02-APR-1999 US 09/286108
PI GORDON W DUFF, FRANCESCO SAVERIO DI GIOVINE, MORTA WHITE PC
C12N15/09, A61K31/57, A61K31/7088, A61K38/00, A61K45/00, A61K48/00, PC
A61P11/00,
PC C12Q1/02, C12Q1/68, G01N33/15, G01N33/50, G01N33/53, G01N33/566, PC
C12N15/00
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Best Local Similarity 100.0%; Pred. No. 8;
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Qy 1 CTCAGCAACACTCCTAT 17
Db 1 CTCAGCAACACTCCTAT 17

INTERLEUKIN GENETICS INC
OS Artificial Sequence
PN JP 2002533096-A/1
PD 08-OCT-2002
PF 01-NOV-1999 JP 2000589732
PR 30-OCT-1998 US 09/183850
PI FRANCESCO S DI GIOVINE, GORDON W DUFF
PC C12N15/09, A61K38/00, A61K45/00, A61P31/00, C12Q1/68, C12N15/00, PC
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Db 1 CTCAGCAACACTCCTAT 17

RESULT 9
CQ918145
LOCUS CQ918145 17 bp DNA linear PAT 23-NOV-2004
DEFINITION Sequence 29 from Patent WO2004097045.
ACCESSION CQ918145
VERSION CQ918145.1 GI:56208292
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Brown, M.A.
TITLE Diagnostic assay for ankylosing spondylitis
JOURNAL Patent: WO 2004097045-A 29 11-NOV-2004;
ISIS INNOVATION LIMITED (GB)
FEATURES
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            /db_xref="taxon:32630"
            /note="Primer"
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Best Local Similarity 100.0%; Pred. No. 8;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTCAGCAACACTCCTAT 17
Db 1 CTCAGCAACACTCCTAT 17

RESULT 10
CS231184
LOCUS CS231184 17 bp DNA linear PAT 15-DEC-2005
DEFINITION Sequence 22 from Patent WO2005108619.
ACCESSION CS231184
VERSION CS231184.1 GI:83698459
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Duff, G.W.
TITLE Diagnostics and therapeutics for diseases associated with an
il-1inflammatory haplotype
JOURNAL Patent: WO 2005108619-A 22 17-NOV-2005;
Interleukin Genetics, Inc. (US)
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Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 CTCAGCAACACTCCTAT 17

RESULT 11
AR282877
LOCUS AR282877 17 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 1 from patent US 6524795.
ACCESSION AR282877
VERSION AR282877.1 GI:29719679
KEYWORDS Unknown.
SOURCE Unknown.

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Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Francis, S.E., Crossman, D.C., Duff, G.W., Kornman, K.S. and Stephenson, K.
TITLE Diagnostics for cardiovascular disorders
JOURNAL Patent: US 6524795-A 1 25-FEB-2003;
FEATURES Location/Qualifiers
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/mol_type="genomic DNA"

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Best Local Similarity 100.0%; Pred. No. 8;
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Qy 1 CTCAGCAACTCCTAT 17
Db 1 CTCAGCAACTCCTAT 17

RESULT 12
185578 I85578 17 bp DNA linear PAT 10-JUN-1998
LOCUS Sequence 1 from patent US 5698399.
DEFINITION I85578
ACCESSION I85578
VERSION I85578.1 GI:3205296
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Duff, G.W., Russell, G. and Eastell, R.
TITLE Detecting genetic predisposition for osteoporosis
JOURNAL Patent: US 5698399-A 1 16-DEC-1997;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"

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Best Local Similarity 100.0%; Pred. No. 8;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCAGCAACTCCTAT 17
Db 1 CTCAGCAACTCCTAT 17

RESULT 13
AR487085 AR487085 17 bp DNA linear PAT 14-MAY-2004
LOCUS Sequence 22 from patent US 6706478.
DEFINITION AR487085
ACCESSION AR487085
VERSION AR487085.1 GI:47252036
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Duff, G.W., Cox, A., Camp, N.J. and di Giovine, F.S.
TITLE Diagnostics and therapeutics for diseases associated with an IL-1 inflammatory haplotype
JOURNAL Patent: US 6706478-A 22 16-MAR-2004;
Interleukin Genetics, Inc.; Waltham, MA;
GBX;
FEATURES Location/Qualifiers
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/mol_type="genomic DNA"

Query Match 100.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 CTCAGCAACTCCTAT 17
Db 1 CTCAGCAACTCCTAT 17

RESULT 14
AR490513 AR490513 17 bp DNA linear PAT 15-MAY-2004
LOCUS Sequence 5 from patent US 6713253.
DEFINITION AR490513
ACCESSION AR490513
VERSION AR490513.1 GI:47257894
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Duff, G.W., Richardson, P.R.S. and Rennie, I.G.
TITLE Detecting genetic predisposition to sight-threatening diabetic retinopathy
JOURNAL Patent: US 6713253-A 5 30-MAR-2004;
Interleukin Genetics, Inc.; Waltham, MA;
GBX;
FEATURES Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 8;
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Qy 1 CTCAGCAACTCCTAT 17
Db 1 CTCAGCAACTCCTAT 17

RESULT 15
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LOCUS Sequence 7 from patent US 6720141.
DEFINITION AR493814
ACCESSION AR493814
VERSION AR493814.1 GI:47266264
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Crossman, D.C., Duff, G.W., Francis, S.E., Kornman, K.S. and Stephenson, K.
TITLE Diagnostics and therapeutics for restenosis
JOURNAL Patent: US 6720141-A 7 13-APR-2004;
Interleukin Genetics, Inc.; Waltham, MA
FEATURES Location/Qualifiers
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Query Match 100.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCAGCAACTCCTAT 17
Db 1 CTCAGCAACTCCTAT 17

RESULT 16
AR532946 AR532946 17 bp DNA linear PAT 08-OCT-2004
LOCUS Sequence 9 from patent US 6730476.
DEFINITION AR532946
ACCESSION AR532946
VERSION AR532946.1 GI:53922498

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[illegible]



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AX067286
LOCUS AX067286 17 bp DNA linear PAT 24-JAN-2001
DEFINITION Sequence 22 from Patent WO0100880.
ACCESSION AX067286
VERSION AX067286.1 GI:12544910
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
AUTHORS Duff,G.W., Cox,A., Camp,N.J. and di Giovine,F.S.
TITLE Diagnostics and therapeutics for diseases associated with an il-1
inflammatory haplotype
JOURNAL Patent: WO 0100880-A 22 04-JAN-2001;
Interleukin Genetics, Inc. (US)
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/db_xref="taxon:32630"
/note="primer"

Query Match 100.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCAGCAACTCCTAT 17
Db |||||

RESULT 22
AX360017
LOCUS AX360017 17 bp DNA linear PAT 13-FEB-2002
DEFINITION Sequence 3 from Patent WO2000933.
ACCESSION AX360017
VERSION AX360017.1 GI:18675643
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
AUTHORS Duff,G.W. and Kornman,K.S.
TITLE Screening assays for identifying modulators of the inflammatory or
immune responses
JOURNAL Patent: WO 0200933-A 3 03-JAN-2002;
Interleukin Genetics, Inc. (US)
FEATURES
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match 100.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCAGCAACTCCTAT 17
Db |||||

RESULT 23
AR045302/c
LOCUS AR045302 15 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 95 from patent US 5817796.
ACCESSION AR045302
VERSION AR045302.1 GI:5966767
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.

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REFERENCE 1 (bases 1 to 15)
AUTHORS Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
TITLE C-myb ribozymes having 2'-5'-linked adenylylate residues
JOURNAL Patent: US 5817796-A 95 06-OCT-1998;
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Best Local Similarity 85.7%; Pred. No. 47;
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QY 1 CTCAGCAACTCC 14
Db |||||

RESULT 24
IS2354
LOCUS IS2354 15 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 95 from patent US 5646042.
ACCESSION IS2354
VERSION IS2354.1 GI:2473555
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
TITLE C-myb targeted ribozymes
JOURNAL Patent: US 5646042-A 95 08-JUL-1997;
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QY 1 CTCAGCAACTCC 14
Db |||||

RESULT 25
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LOCUS AX587048/c 15 bp DNA linear PAT 10-JAN-2003
DEFINITION Sequence 70 from Patent WO02072883.
ACCESSION AX587048
VERSION AX587048.1 GI:27655923
KEYWORDS Saccharomyces cerevisiae (baker's yeast)
SOURCE Saccharomyces cerevisiae
ORGANISM Saccharomyces cerevisiae
REFERENCE 1
AUTHORS Roetger,A.
TITLE Nucleotide carrier for diagnosing and treating oral diseases
JOURNAL Patent: WO 02072883-A 70 19-SEP-2002;
Roetger, Antje (DE)
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QY 4 AGCAACTCCTAT 17

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RESULT 30
AR301565/c
LOCUS AR301565 11 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 146 from patent US 6538173.
ACCESSION AR301565
VERSION AR301565.1 GI:31689367
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 11)
AUTHORS Heber-Katz, E.
TITLE Compositions and methods for wound healing
JOURNAL Patent: US 6538173-A 146 25-MAR-2003;
The Wistar Institute; Philadelphia, PA;
WOK;
FEATURES
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/mol_type="genomic DNA"
Query Match 52.9%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTCAGCAAC 9
Db 9 CTCAGCAAC 1
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RESULT 31
AR322159
LOCUS AR322159 12 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 10 from patent US 6566061.
ACCESSION AR322159
VERSION AR322159.1 GI:33707703
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 12)
AUTHORS Philibert, R.A., Gimms, E.I. and Delisi, L.
TITLE Identification of polymorphisms in the PCTG4 region of Xq13
JOURNAL Patent: US 6566061-A 10 20-MAY-2003;
The University of Iowa, as represented by the University of Iowa
Research Foundation and The United States of America as represented
by the Department of Health and Human Services; Iowa City, IA
FEATURES
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Best Local Similarity 100.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 CAGCAACAC 11
Db 1 CAGCAACAC 9
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RESULT 32
BD239508
LOCUS BD239508 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD239508
VERSION BD239508.1 GI:33049278
KEYWORDS JP 2002534056-A/926.
SOURCE Homo sapiens (human).
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE
1 (bases 1 to 10)
AUTHORS Roberts, B.L. and Shankara, S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 1028 15-OCT-2002;
GENZYME CORP
COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/1028
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039, 19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041, 19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089997, 19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035, 19-JUN-1998 US 60/089993 PR
19-JUN-1998 US 60/089992, 19-JUN-1998 US 60/090072 PR
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19-JUN-1998 US 60/089994, 19-JUN-1998 US 60/090077 PR
19-JUN-1998 US 60/090078, 19-JUN-1998 US 60/090047 PR
19-JUN-1998 US 60/090076, 19-JUN-1998 US 60/090045 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS, SRINIVAS SHANKARA
PC C12N15/09, C12N15/09, A61K39/00, A61P35/00, A61P37/04, C12N1/15, PC
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PC C12N1/21, C12N5/10, G01N33/15, G01N33/50, G01N33/53, G01N33/566, PC
G01N37/00,
PC C12N15/00, C12N5/00, C12N15/00
CC Preparation and use of superior vaccines
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Location/Qualifiers
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Best Local Similarity 90.0%; Pred. No. 41;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CTCAGCAACA 10
Db 1 CTCAGCAAAA 10
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RESULT 33
BD239610/c
LOCUS BD239610 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD239610
VERSION BD239610.1 GI:33049380
KEYWORDS JP 2002534056-A/1028.
SOURCE Homo sapiens (human).
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE
1 (bases 1 to 10)
AUTHORS Roberts, B.L. and Shankara, S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 1028 15-OCT-2002;
GENZYME CORP
COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/1028
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039, 19-JUN-1998 US 60/090040 PR
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19-JUN-1998 US 60/090079, 19-JUN-1998 US 60/090079 PR

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19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
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19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
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19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
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08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS, SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
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PC C12N15/00,C12N5/00,C12N15/00
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FH Key Location/Qualifiers
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/db_xref="taxon:9606"

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Best Local Similarity 90.0%; Pred. No. 41;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTCAGCAACA 10
Db 10 CTCAGCAACA 1

RESULT 34
CQ944980
LOCUS
DEFINITION Sequence 127 from Patent WO2004099445.
ACCESSION CQ944980
VERSION CQ944980.1 GI:56294321
KEYWORDS
ORGANISM synthetic construct
SOURCE synthetic construct
OTHER SEQUENCES; artificial sequences.
REFERENCE 1
AUTHORS Kahl,G., Winter,P., Krueger,D., Reich,S., Matsumura,H. and Terauchi,R.
TITLE Use of a type iii restriction enzyme to isolate identification tags comprising more than 25 nucleotides
JOURNAL Patent: WO 2004099445-A 127 18-NOV-2004; Iwate Prefectural Government (JP)
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/notes="Description of Artificial Sequence:Synthetic DNA (Tag Sequence)"

Query Match 49.4%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 41;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CAGCAACT 12
Db 1 CAGCAACT 10

RESULT 35
AX153002
LOCUS
DEFINITION Sequence 917 from Patent WO0138577.
ACCESSION AX153002
VERSION AX153002.1 GI:14534653
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 917 31-MAY-2001; The Johns Hopkins University (US)
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Query Match 49.4%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 41;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CAACACTCTCT 15
Db 1 CAACACTCTCT 10

RESULT 36
AX377359
LOCUS
DEFINITION Sequence 23 from Patent WO212499.
ACCESSION AX377359
VERSION AX377359.1 GI:19573645
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Kliem,S.B., Koshiy,B. and Lanz,E.M.
TITLE Haplotypes of the nt3 gene
JOURNAL Patent: WO 0212499-A 23 14-FEB-2002; Genessee Pharmaceuticals, Inc. (US)
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Query Match 49.4%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 41;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GCAACACTCTCC 14
Db 1 GCAACACTCTCC 10

RESULT 37
CQ832726/c
LOCUS
DEFINITION Sequence 97 from Patent WO2004059002.
ACCESSION CQ832726
VERSION CQ832726.1 GI:50832333
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

```

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Hominidae; Homo.
1
REFERENCE
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
Conrad,M. and Hofmann,K.
TITLE Method for determining the homeostasis of hairy skin
JOURNAL Patent: WO 2004059002-A 97 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
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/organism="Homo sapiens"
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Query Match 49.4%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 CTCAGCAACA 10
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Db 11 CCCAGCAACA 2

RESULT 38
CQ833174/c
LOCUS CQ833174 11 bp DNA linear PAT 29-JUL-2004
DEFINITION Sequence 545 from Patent WO2004059002.
ACCESSION CQ833174
VERSION CQ833174.1 GI:50832781
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
Conrad,M. and Hofmann,K.
TITLE Method for determining the homeostasis of hairy skin
JOURNAL Patent: WO 2004059002-A 545 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
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source Location/Qualifiers
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/db_xref="taxon:9606"
Query Match 49.4%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 3 CAGCAACT 12
| | | | | | | |
Db 10 CAGCAACT 1

RESULT 39
CQ835198
LOCUS CQ835198 11 bp DNA linear PAT 29-JUL-2004
DEFINITION Sequence 256 from Patent WO2004059001.
ACCESSION CQ835198
VERSION CQ835198.1 GI:50834732
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
Conrad,M. and Hofmann,K.
TITLE Method for determining markers of human facial skin
JOURNAL Patent: WO 2004059001-A 256 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
Hominidae; Homo.
1
REFERENCE
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
Conrad,M. and Hofmann,K.
TITLE Method for determining hair cycle markers
JOURNAL Patent: WO 2005028671-A 229 31-MAR-2005;
Henkel Kommanditgesellschaft auf Aktien (DE)
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source Location/Qualifiers
1..11
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/mol_type="unassigned DNA"
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Query Match 49.4%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 5 GCAACACTCC 14
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Db 1 GCAAACTCC 10

RESULT 40
CS058107
LOCUS CS058107 11 bp DNA linear PAT 13-APR-2005
DEFINITION Sequence 4 from Patent WO2005028671.
ACCESSION CS058107
VERSION CS058107.1 GI:62551059
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS Holtkoetter,O., Petersohn,D., Schlotmann,K., Giesen,M. and
Kessler-Becker,D.
TITLE Method for determining hair cycle markers
JOURNAL Patent: WO 2005028671-A 4 31-MAR-2005;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source Location/Qualifiers
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Oy 6 CAACACTCCT 15
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Db 1 CAACACTCCT 10

RESULT 41
CS058332
LOCUS CS058332 11 bp DNA linear PAT 13-APR-2005
DEFINITION Sequence 229 from Patent WO2005028671.
ACCESSION CS058332
VERSION CS058332.1 GI:62551515
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS Holtkoetter,O., Petersohn,D., Schlotmann,K., Giesen,M. and
Kessler-Becker,D.
TITLE Method for determining hair cycle markers
JOURNAL Patent: WO 2005028671-A 229 31-MAR-2005;
Henkel Kommanditgesellschaft auf Aktien (DE)
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source Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Best Local Similarity 90.0%; Pred. No. 51;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CAACACTCCT 15  
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Db 1 CAACATTCCT 10

RESULT 42  
AX623499  
LOCUS AX623499 11 bp DNA linear PAT 21-FEB-2003  
DEFINITION Sequence 540 from Patent WO02053774.  
ACCESSION AX623499  
VERSION AX623499.1 GI:28451440  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM

REFERENCE  
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.  
TITLE Method for determining homeostasis of the skin  
JOURNAL Patent: WO 02053774-A 540 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
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Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GCAACACTCC 14  
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Db 1 GCAAGACTCC 10

RESULT 43  
AX624606  
LOCUS AX624606 11 bp DNA linear PAT 21-FEB-2003  
DEFINITION Sequence 1647 from Patent WO02053774.  
ACCESSION AX624606  
VERSION AX624606.1 GI:28452547  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM

REFERENCE  
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.  
TITLE Method for determining homeostasis of the skin  
JOURNAL Patent: WO 02053774-A 1647 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
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source Location/Qualifiers  
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Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 AACACTCCTA 16  
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Db 1 AACATTCCTA 10

RESULT 44  
AX627166  
LOCUS AX627166 11 bp DNA linear PAT 21-FEB-2003  
DEFINITION Sequence 4207 from Patent WO02053774.  
ACCESSION AX627166  
VERSION AX627166.1 GI:28455204  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM

Query Match 49.4%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 51;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

AX624745  
LOCUS AX624745 11 bp DNA linear PAT 21-FEB-2003  
DEFINITION Sequence 1786 from Patent WO02053774.  
ACCESSION AX624745  
VERSION AX624745.1 GI:28452686  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM

REFERENCE  
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.  
TITLE Method for determining homeostasis of the skin  
JOURNAL Patent: WO 02053774-A 1786 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
FEATURES  
source Location/Qualifiers  
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Query Match 49.4%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 51;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 AGCAACACTC 13  
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Db 1 AGAAACACTC 10

RESULT 45  
AX626573  
LOCUS AX626573 11 bp DNA linear PAT 21-FEB-2003  
DEFINITION Sequence 3614 from Patent WO02053774.  
ACCESSION AX626573  
VERSION AX626573.1 GI:28454611  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM

REFERENCE  
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.  
TITLE Method for determining homeostasis of the skin  
JOURNAL Patent: WO 02053774-A 3614 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
FEATURES  
source Location/Qualifiers  
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Query Match 49.4%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 51;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CAACACTCCT 15  
| | | | |  
Db 1 CAACATTCCT 10

RESULT 46  
AX627166  
LOCUS AX627166 11 bp DNA linear PAT 21-FEB-2003  
DEFINITION Sequence 4207 from Patent WO02053774.  
ACCESSION AX627166  
VERSION AX627166.1 GI:28455204  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM

Query Match 49.4%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 51;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CAACACTCCT 15  
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Db 1 CAACATTCCT 10

RESULT 47  
AX627166  
LOCUS AX627166 11 bp DNA linear PAT 21-FEB-2003  
DEFINITION Sequence 4207 from Patent WO02053774.  
ACCESSION AX627166  
VERSION AX627166.1 GI:28455204  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM

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Qy 6 CAACACTCCT 15  
| | | | |  
Db 1 CAACATTCCT 10

RESULT 48  
AX627166  
LOCUS AX627166 11 bp DNA linear PAT 21-FEB-2003  
DEFINITION Sequence 4207 from Patent WO02053774.  
ACCESSION AX627166  
VERSION AX627166.1 GI:28455204  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM

Query Match 49.4%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 51;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CAACACTCCT 15  
| | | | |  
Db 1 CAACATTCCT 10

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

## REFERENCE

AUTHORS Petersohn,D., Conrad,M. and Hofmann,K.  
TITLE Method for determining homeostasis of the skin  
JOURNAL Patent: WO 02053774-A 4207 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)

## FEATURES

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Query Match 49.4%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 51;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

## QY

6 CAACACTCTCCT 15

1 CAGCACTCTCCT 10

RESULT 47  
AX630920  
LOCUS AX630920 11 bp DNA linear PAT 21-FEB-2003  
DEFINITION Sequence 7961 from Patent WO02053774.  
ACCESSION AX630920  
VERSION AX630920.1 GI:28458960  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

## REFERENCE

AUTHORS Petersohn,D., Conrad,M. and Hofmann,K.  
TITLE Method for determining homeostasis of the skin  
JOURNAL Patent: WO 02053774-A 7961 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)

## FEATURES

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Query Match 49.4%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 51;  
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## QY

5 GCAACACTCTC 14

1 GCAAGACTCC 10

RESULT 48  
AX632027  
LOCUS AX632027 11 bp DNA linear PAT 21-FEB-2003  
DEFINITION Sequence 9069 from Patent WO02053774.  
ACCESSION AX632027  
VERSION AX632027.1 GI:28467642  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

## REFERENCE

AUTHORS Petersohn,D., Conrad,M. and Hofmann,K.  
TITLE Method for determining homeostasis of the skin  
JOURNAL Patent: WO 02053774-A 9069 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)

## FEATURES

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Best Local Similarity 90.0%; Pred. No. 51;  
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## QY

7 AACACTCTCTA 16

1 AACATTCTTA 10

RESULT 49  
AX632166  
LOCUS AX632166 11 bp DNA linear PAT 21-FEB-2003  
DEFINITION Sequence 9208 from Patent WO02053774.  
ACCESSION AX632166  
VERSION AX632166.1 GI:28467781  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

## REFERENCE

AUTHORS Petersohn,D., Conrad,M. and Hofmann,K.  
TITLE Method for determining homeostasis of the skin  
JOURNAL Patent: WO 02053774-A 9208 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)

## FEATURES

Location/Qualifiers  
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/db\_xref="taxon:9606"

Query Match 49.4%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 51;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

## QY

4 AGCAACACTC 13

1 AGAAACACTC 10

RESULT 50  
AX708088/c  
LOCUS AX708088 11 bp DNA linear PAT 04-APR-2003  
DEFINITION Sequence 24 from Patent WO03014387.  
ACCESSION AX708088  
VERSION AX708088.1 GI:29564039  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

## REFERENCE

AUTHORS Wojnowski,L. and Presecan-Siedel,E.  
TITLE Polymorphisms in the human gene for cypla2 and their use in  
JOURNAL Patent: WO 03014387-A 24 20-FEB-2003;  
Epidauros Biotechnologie AG (DE)

## FEATURES

Location/Qualifiers  
1. .11  
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Query Match 49.4%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 51;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

## QY

8 ACACCTCCTAT 17

1111111111

Db 10 ACCCTCTAT 1

Search completed: November 21, 2006, 14:27:36  
Job time : 1 secs





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112	9.4	55.3	12	1	ABI70277	Oligonucleotide pr	c 185	9.4	55.3	13	1	ABC71080	Oligonucleotide SE
c 113	9.4	55.3	12	1	ABI32479	Oligonucleotide pr	c 186	9.4	55.3	13	1	ABC24579	Oligonucleotide SE
c 114	9.4	55.3	12	1	ABH83410	Oligonucleotide pr	c 187	9.4	55.3	13	1	ABC86466	Oligonucleotide SE
c 115	9.4	55.3	12	1	ABH87181	Oligonucleotide pr	c 188	9.4	55.3	13	1	ABF32704	Oligonucleotide SE
116	9.4	55.3	12	1	ABI51414	Oligonucleotide pr	c 189	9.4	55.3	13	1	ABH33143	Oligonucleotide SE
117	9.4	55.3	12	1	ABH82860	Oligonucleotide pr	c 190	9.4	55.3	13	1	ABC42724	Oligonucleotide SE
c 118	9.4	55.3	12	1	ABI38024	Oligonucleotide pr	c 191	9.4	55.3	13	1	ABC00318	Oligonucleotide SE
c 119	9.4	55.3	12	1	ABI21294	Oligonucleotide pr	c 192	9.4	55.3	13	1	ABC25801	Oligonucleotide SE
c 120	9.4	55.3	12	1	ABI21379	Oligonucleotide pr	c 193	9.4	55.3	13	1	ABF27385	Oligonucleotide SE
121	9.4	55.3	12	1	ABI15864	Oligonucleotide pr	c 194	9.4	55.3	13	1	ABF73020	Oligonucleotide SE
122	9.4	55.3	12	1	ABI69688	Oligonucleotide pr	c 195	9.4	55.3	13	1	ABH26572	Oligonucleotide SE
c 123	9.4	55.3	12	1	ABH80014	Oligonucleotide pr	c 196	9.4	55.3	13	1	ABH48700	Oligonucleotide SE
c 124	9.4	55.3	12	1	ABI79343	Oligonucleotide pr	c 197	9.4	55.3	13	1	ABC96629	Oligonucleotide SE
c 125	9.4	55.3	13	1	ABF04402	Oligonucleotide SE	c 198	9.4	55.3	13	1	ABC25800	Oligonucleotide SE
c 126	9.4	55.3	13	1	ABF69369	Oligonucleotide SE	c 199	9.4	55.3	13	1	ABC78901	Oligonucleotide SE
c 127	9.4	55.3	13	1	ABH27108	Oligonucleotide SE	c 200	9.4	55.3	13	1	ABC62432	Oligonucleotide SE
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c 137	9.4	55.3	13	1	ABH07982	Oligonucleotide SE	c 210	9.4	55.3	13	1	ABC75387	Oligonucleotide SE
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c 144	9.4	55.3	13	1	ABF69368	Oligonucleotide SE	c 217	9.4	55.3	13	1	ABH333248	Oligonucleotide SE
c 145	9.4	55.3	13	1	ABF73021	Oligonucleotide SE	c 218	9.4	55.3	13	1	ABH333248	Oligonucleotide SE
c 146	9.4	55.3	13	1	ABH35026	Oligonucleotide SE	c 219	9.4	55.3	13	1	ABH333248	Oligonucleotide SE
c 147	9.4	55.3	13	1	ABF08236	Oligonucleotide SE	c 220	9.4	55.3	13	1	ABF39825	Oligonucleotide SE
c 148	9.4	55.3	13	1	ABF08236	Oligonucleotide SE	c 221	9.4	55.3	13	1	AAF41735	Oligonucleotide SE
c 149	9.4	55.3	13	1	ABC39628	Oligonucleotide SE	c 222	9.4	55.3	13	1	AAF41735	Oligonucleotide SE
c 150	9.4	55.3	13	1	ABF27388	Oligonucleotide SE	c 223	9.4	55.3	13	1	AAF41735	Oligonucleotide SE
c 151	9.4	55.3	13	1	ABF53293	Oligonucleotide SE	c 224	9.4	55.3	13	1	AAF41735	Oligonucleotide SE
c 152	9.4	55.3	13	1	ABH33142	Oligonucleotide SE	c 225	9.4	55.3	13	1	AAF41735	Oligonucleotide SE
c 153	9.4	55.3	13	1	ABC50881	Oligonucleotide SE	c 226	9.4	55.3	13	1	AAF41735	Oligonucleotide SE
154	9.4	55.3	13	1	ABF17655	Oligonucleotide SE	c 227	9.4	55.3	13	1	AAF41735	Oligonucleotide SE
c 155	9.4	55.3	13	1	ABF32705	Oligonucleotide SE	c 228	9.4	55.3	13	1	AAF41735	Oligonucleotide SE
c 156	9.4	55.3	13	1	ABF36019	Oligonucleotide SE	c 229	9.4	55.3	13	1	AAF41735	Oligonucleotide SE
c 157	9.4	55.3	13	1	ABH00132	Oligonucleotide SE	c 230	9.4	55.3	13	1	AAF41735	Oligonucleotide SE
c 158	9.4	55.3	13	1	ABH00133	Oligonucleotide SE	c 231	9.4	55.3	13	1	AAF41735	Oligonucleotide SE
c 159	9.4	55.3	13	1	ABH11456	Oligonucleotide SE	c 232	9.4	55.3	13	1	AAF41735	Oligonucleotide SE
c 160	9.4	55.3	13	1	ABH11457	Oligonucleotide SE	c 233	9.4	55.3	13	1	AAF41735	Oligonucleotide SE
c 161	9.4	55.3	13	1	ABF90352	Oligonucleotide SE	c 234	9.4	55.3	13	1	AAF41735	Oligonucleotide SE
c 162	9.4	55.3	13	1	ABC96628	Oligonucleotide SE	c 235	9.4	55.3	13	1	AAF41735	Oligonucleotide SE
c 163	9.4	55.3	13	1	ABC50880	Oligonucleotide SE	c 236	9.4	55.3	13	1	AAF41735	Oligonucleotide SE
c 164	9.4	55.3	13	1	ABF36018	Oligonucleotide SE	c 237	9.4	55.3	13	1	AAF41735	Oligonucleotide SE
c 165	9.4	55.3	13	1	ABF79045	Oligonucleotide SE	c 238	9.4	55.3	13	1	AAF41735	Oligonucleotide SE
c 166	9.4	55.3	13	1	ABF53999	Oligonucleotide SE	c 239	9.4	55.3	13	1	AAF41735	Oligonucleotide SE
c 167	9.4	55.3	13	1	ABH59111	Oligonucleotide SE	c 240	9.4	55.3	13	1	AAF41735	Oligonucleotide SE
c 168	9.4	55.3	13	1	ABC71081	Oligonucleotide SE	c 241	9.4	55.3	13	1	AAF41735	Oligonucleotide SE
c 169	9.4	55.3	13	1	ABC47373	Oligonucleotide SE	c 242	9.4	55.3	13	1	AAF41735	Oligonucleotide SE
c 170	9.4	55.3	13	1	ABC86465	Oligonucleotide SE	c 243	9.4	55.3	13	1	AAF41735	Oligonucleotide SE
c 171	9.4	55.3	13	1	ABH27109	Oligonucleotide SE	c 244	9.4	55.3	13	1	AAF41735	Oligonucleotide SE
c 172	9.4	55.3	13	1	ABF53292	Oligonucleotide SE	c 245	9.4	55.3	13	1	AAF41735	Oligonucleotide SE
c 173	9.4	55.3	13	1	ABH07983	Oligonucleotide SE	c 246	9.4	55.3	13	1	AAF41735	Oligonucleotide SE
c 174	9.4	55.3	13	1	ABH86467	Oligonucleotide SE	c 247	9.4	55.3	13	1	AAF41735	Oligonucleotide SE
c 175	9.4	55.3	13	1	ABF78085	Oligonucleotide SE	c 248	9.4	55.3	13	1	AAF41735	Oligonucleotide SE
c 176	9.4	55.3	13	1	ABC00319	Oligonucleotide SE	c 249	9.4	55.3	13	1	AAF41735	Oligonucleotide SE
c 177	9.4	55.3	13	1	ABF90353	Oligonucleotide SE	c 250	9.4	55.3	13	1	AAF41735	Oligonucleotide SE
c 178	9.4	55.3	13	1	ABF71075	Oligonucleotide SE	c 251	9.4	55.3	13	1	AAF41735	Oligonucleotide SE
c 179	9.4	55.3	13	1	ABF71084	Oligonucleotide SE	c 252	9.4	55.3	13	1	AAF41735	Oligonucleotide SE

C 253	8.8	51.8	12	1	ABI74519	Oligonucleotide pr
C 254	8.8	51.8	12	1	ABI71780	Oligonucleotide pr
C 255	8.8	51.8	12	1	ABI07523	Oligonucleotide pr
C 256	8.8	51.8	12	1	ABI51318	Oligonucleotide pr
C 257	8.8	51.8	12	1	ABI21119	Oligonucleotide pr
C 258	8.8	51.8	12	1	ABI26465	Oligonucleotide pr
C 259	8.8	51.8	12	1	ABI29621	Oligonucleotide pr
C 260	8.8	51.8	12	1	ABI13441	Oligonucleotide pr
C 261	8.8	51.8	12	1	ABI67962	Oligonucleotide pr
C 262	8.8	51.8	12	1	ABI32800	Oligonucleotide pr
C 263	8.8	51.8	12	1	ABI52724	Oligonucleotide pr
C 264	8.8	51.8	12	1	ABI57315	Oligonucleotide pr
C 265	8.8	51.8	12	1	ABI70146	Oligonucleotide pr
C 266	8.8	51.8	12	1	ABH95774	Oligonucleotide pr
C 267	8.8	51.8	12	1	ABH98439	Oligonucleotide pr
C 268	8.8	51.8	12	1	ABH77746	Oligonucleotide pr
C 269	8.8	51.8	12	1	ABI62490	Oligonucleotide pr
C 270	8.8	51.8	12	1	ABI79845	Oligonucleotide pr
C 271	8.8	51.8	12	1	ABI79880	Oligonucleotide pr
C 272	8.8	51.8	12	1	ABI28200	Oligonucleotide pr
C 273	8.8	51.8	12	1	ABI52706	Oligonucleotide pr
C 274	8.8	51.8	12	1	ABI75840	Oligonucleotide pr
C 275	8.8	51.8	12	1	ABI07459	Oligonucleotide pr
C 276	8.8	51.8	12	1	ABH90883	Oligonucleotide pr
C 277	8.4	49.4	10	1	AAZ78498	Human dendritic ce
C 278	8.4	49.4	10	1	AAZ78600	Human dendritic ce
C 279	8.4	49.4	10	1	AAZ86614	Metastatic breast
C 280	8.4	49.4	10	1	AAZ84155	Metastatic breast
C 281	8.4	49.4	10	1	AAZ81494	Metastatic breast
C 282	8.4	49.4	10	1	AAZ84891	Metastatic breast
C 283	8.4	49.4	10	1	AAZ85466	Metastatic breast
C 284	8.4	49.4	10	1	AAZ85411	Metastatic breast
C 285	8.4	49.4	10	1	AAZ84473	Metastatic breast
C 286	8.4	49.4	10	1	AAH64077	Human ubiqutously
C 287	8.4	49.4	10	1	AAF35663	Yeast NORF gene SA
C 288	8.4	49.4	10	1	AAF37497	Yeast NORF gene SA
C 289	8.4	49.4	10	1	AAF34369	Yeast NORF gene SA
C 290	8.4	49.4	10	1	AAF40845	Yeast NORF gene SA
C 291	8.4	49.4	10	1	AAF36364	Yeast NORF gene SA
C 292	8.4	49.4	10	1	AAH18377	Primer-extension o
C 293	8.4	49.4	10	1	ADU182319	Human neurotrophin
C 294	8.4	49.4	10	1	ADU18500	Hypoxia-related tu
C 295	8.4	49.4	10	1	ADU18776	Hypoxia-related tu
C 296	8.4	49.4	10	1	ADU18606	Hypoxia-related tu
C 297	8.4	49.4	10	1	ADU78503	Rice oligonucleoti
C 298	8.4	49.4	11	1	ABV70175	Human skin EST 796
C 299	8.4	49.4	11	1	ABV62754	Human skin EST 540
C 300	8.4	49.4	11	1	ABV63861	Human skin EST 164
C 301	8.4	49.4	11	1	ABV64000	Human skin EST 178
C 302	8.4	49.4	11	1	ABV66421	Human skin EST 420
C 303	8.4	49.4	11	1	ABV71282	Human skin EST 906
C 304	8.4	49.4	11	1	ABV71421	Human skin EST 920
C 305	8.4	49.4	11	1	ABV65828	Human skin EST 361
C 306	8.4	49.4	11	1	ACC90658	Human CYP1A2 PCR p
C 307	8.4	49.4	11	1	ADQ35280	Human hair-bearing
C 308	8.4	49.4	11	1	ADQ35728	Human hair-bearing
C 309	8.4	49.4	11	1	ADQ32166	Human facial skin-
C 310	8.4	49.4	12	1	AAH80290	Oligo HCV-139, tar
C 311	8.4	49.4	12	1	AA241785	Organic material d
C 312	8.4	49.4	12	1	AA241569	Microbe detection
C 313	8.4	49.4	12	1	AAH88508	Gamma-conopeptide
C 314	8.4	49.4	12	1	AAZ34552	Purative Alfini bi
C 315	8.4	49.4	12	1	AAC97920	Primer used to ill
C 316	8.4	49.4	12	1	ABI19922	Oligonucleotide pr
C 317	8.4	49.4	12	1	ABH95281	Oligonucleotide pr
C 318	8.4	49.4	12	1	ABH75072	Oligonucleotide pr
C 319	8.4	49.4	12	1	ABI25291	Oligonucleotide pr
C 320	8.4	49.4	12	1	ABI04562	Oligonucleotide pr
C 321	8.4	49.4	12	1	ABI10726	Oligonucleotide pr
C 322	8.4	49.4	12	1	ABI36250	Oligonucleotide pr
C 323	8.4	49.4	12	1	ABI12735	Oligonucleotide pr
C 324	8.4	49.4	12	1	ABI73353	Oligonucleotide pr
C 325	8.4	49.4	12	1	ABI79465	Oligonucleotide pr

C 326	8.4	49.4	12	1	ABI20130	Oligonucleotide pr
C 327	8.4	49.4	12	1	ABI04273	Oligonucleotide pr
C 328	8.4	49.4	12	1	ABI32048	Oligonucleotide pr
C 329	8.4	49.4	12	1	ABI49461	Oligonucleotide pr
C 330	8.4	49.4	12	1	ABI50359	Oligonucleotide pr
C 331	8.4	49.4	12	1	ABI71640	Oligonucleotide pr
C 332	8.4	49.4	12	1	ABI58376	Oligonucleotide pr
C 333	8.4	49.4	12	1	ABI60263	Oligonucleotide pr
C 334	8.4	49.4	12	1	ABH85930	Oligonucleotide pr
C 335	8.4	49.4	12	1	ABI37591	Oligonucleotide pr
C 336	8.4	49.4	12	1	ABI49460	Oligonucleotide pr
C 337	8.4	49.4	12	1	ABI73802	Oligonucleotide pr
C 338	8.4	49.4	12	1	ABI23841	Oligonucleotide pr
C 339	8.4	49.4	12	1	ABH75074	Oligonucleotide pr
C 340	8.4	49.4	12	1	ABI26596	Oligonucleotide pr
C 341	8.4	49.4	12	1	ABI02634	Oligonucleotide pr
C 342	8.4	49.4	12	1	ABI05684	Oligonucleotide pr
C 343	8.4	49.4	12	1	ABI35125	Oligonucleotide pr
C 344	8.4	49.4	12	1	ABH85359	Oligonucleotide pr
C 345	8.4	49.4	12	1	ABI60784	Oligonucleotide pr
C 346	8.4	49.4	12	1	ABI62460	Oligonucleotide pr
C 347	8.4	49.4	12	1	ABH75244	Oligonucleotide pr
C 348	8.4	49.4	12	1	ABI08676	Oligonucleotide pr
C 349	8.4	49.4	12	1	ABH86879	Oligonucleotide pr
C 350	8.4	49.4	12	1	ABH89347	Oligonucleotide pr
C 351	8.4	49.4	12	1	ABI51514	Oligonucleotide pr
C 352	8.4	49.4	12	1	ABI52940	Oligonucleotide pr
C 353	8.4	49.4	12	1	ABI78050	Oligonucleotide pr
C 354	8.4	49.4	12	1	ABH83800	Oligonucleotide pr
C 355	8.4	49.4	12	1	ABI52587	Oligonucleotide pr
C 356	8.4	49.4	12	1	ABI65914	Oligonucleotide pr
C 357	8.4	49.4	12	1	ABH68170	Oligonucleotide pr
C 358	8.4	49.4	12	1	ABH71713	Oligonucleotide pr
C 359	8.4	49.4	12	1	ABI23582	Oligonucleotide pr
C 360	8.4	49.4	12	1	ABI23840	Oligonucleotide pr
C 361	8.4	49.4	12	1	ABI29757	Oligonucleotide pr
C 362	8.4	49.4	12	1	ABI35425	Oligonucleotide pr
C 363	8.4	49.4	12	1	ABH89609	Oligonucleotide pr
C 364	8.4	49.4	12	1	ABI52629	Oligonucleotide pr
C 365	8.4	49.4	12	1	ABI73498	Oligonucleotide pr
C 366	8.4	49.4	12	1	ABI76817	Oligonucleotide pr
C 367	8.4	49.4	12	1	ABI77369	Oligonucleotide pr
C 368	8.4	49.4	12	1	ABI65694	Oligonucleotide pr
C 369	8.4	49.4	12	1	ABI81322	Oligonucleotide pr
C 370	8.4	49.4	12	1	ABH71244	Oligonucleotide pr
C 371	8.4	49.4	12	1	ABI02874	Oligonucleotide pr
C 372	8.4	49.4	12	1	ABI04205	Oligonucleotide pr
C 373	8.4	49.4	12	1	ABI54050	Oligonucleotide pr
C 374	8.4	49.4	12	1	ABI61147	Oligonucleotide pr
C 375	8.4	49.4	12	1	ABI62277	Oligonucleotide pr
C 376	8.4	49.4	12	1	ABH93056	Oligonucleotide pr
C 377	8.4	49.4	12	1	ABH94308	Oligonucleotide pr
C 378	8.4	49.4	12	1	ABH71714	Oligonucleotide pr
C 379	8.4	49.4	12	1	ABI01047	Oligonucleotide pr
C 380	8.4	49.4	12	1	ABH80648	Oligonucleotide pr
C 381	8.4	49.4	12	1	ABI13133	Oligonucleotide pr
C 382	8.4	49.4	12	1	ABI42830	Oligonucleotide pr
C 383	8.4	49.4	12	1	ABI68945	Oligonucleotide pr
C 384	8.4	49.4	12	1	ABI62847	Oligonucleotide pr
C 385	8.4	49.4	12	1	ABI04637	Oligonucleotide pr
C 386	8.4	49.4	12	1	ABI33500	Oligonucleotide pr
C 387	8.4	49.4	12	1	ABI35127	Oligonucleotide pr
C 388	8.4	49.4	12	1	ABI36791	Oligonucleotide pr
C 389	8.4	49.4	12	1	ABI42330	Oligonucleotide pr
C 390	8.4	49.4	12	1	ABI72623	Oligonucleotide pr
C 391	8.4	49.4	12	1	ABI64366	Oligonucleotide pr
C 392	8.4	49.4	12	1	ABI79267	Oligonucleotide pr
C 393	8.4	49.4	12	1	ABI80201	Oligonucleotide pr
C 394	8.4	49.4	12	1	ABI02907	Oligonucleotide pr
C 395	8.4	49.4	12	1	ABI34125	Oligonucleotide pr
C 396	8.4	49.4	12	1	ABI37442	Oligonucleotide pr
C 397	8.4	49.4	12	1	ABI42471	Oligonucleotide pr
C 398	8.4	49.4	12	1	ABI47600	Oligonucleotide pr

C 399	8.4	49.4	12	1	ABI54882	Oligonucleotide pr	472	8	47.1	10	1	ABL01209	Human AKR1B1 gene
400	8.4	49.4	12	1	ABI78533	Oligonucleotide pr	473	8	47.1	10	1	ABQ8699	Human CFL1 primer
401	8.4	49.4	12	1	ABH99854	Oligonucleotide pr	c 474	8	47.1	10	1	ACC85197	Human prothrombin
C 402	8.4	49.4	12	1	ABI05412	Oligonucleotide pr	475	8	47.1	10	1	ADU19523	Hypoxia-related tu
C 403	8.4	49.4	12	1	ABI10692	Oligonucleotide pr	476	8	47.1	11	1	AAX24421	Bovine myostatin m
C 404	8.4	49.4	12	1	ABH91733	Oligonucleotide pr	c 477	8	47.1	11	1	ABV64656	Human skin EST 244
405	8.4	49.4	12	1	ABI78665	Oligonucleotide pr	c 478	8	47.1	11	1	ABV66585	Human skin EST 435
406	8.4	49.4	12	1	ABI74449	Oligonucleotide pr	c 479	8	47.1	11	1	ABV71821	Human skin EST 960
C 407	8.4	49.4	12	1	ABI21004	Oligonucleotide pr	480	8	47.1	11	1	ABV65947	Human skin EST 373
C 408	8.4	49.4	12	1	ABH88530	Oligonucleotide pr	c 481	8	47.1	11	1	ABV64400	Human skin EST 218
C 409	8.4	49.4	12	1	ABH89232	Oligonucleotide pr	c 482	8	47.1	11	1	ADQ32942	Human facial skin-
410	8.4	49.4	12	1	ABH89348	Oligonucleotide pr	483	8	47.1	11	1	ADQ33462	Human facial skin-
C 411	8.4	49.4	12	1	ABI39892	Oligonucleotide pr	484	8	47.1	11	1	ADR35386	Human nicking agen
C 412	8.4	49.4	12	1	ABI15535	Oligonucleotide pr	485	8	47.1	11	1	ADR35383	Human nicking agen
C 413	8.4	49.4	12	1	ABI42757	Oligonucleotide pr	486	8	47.1	11	1	ADR35385	Human nicking agen
C 414	8.4	49.4	12	1	ABI56889	Oligonucleotide pr	487	8	47.1	11	1	ADR35384	Human nicking agen
415	8.4	49.4	12	1	ABI59223	Oligonucleotide pr	488	8	47.1	11	1	AD223301	Human SNP detectio
416	8.4	49.4	12	1	ABI75721	Oligonucleotide pr	c 489	7.8	45.9	11	1	ABQ87409	Human skin stress/
417	8.4	49.4	12	1	ABI62250	Oligonucleotide pr	c 490	7.8	45.9	11	1	ABQ86733	Human skin stress/
C 418	8.4	49.4	12	1	ABI78281	Oligonucleotide pr	c 491	7.8	45.9	11	1	ABV66019	Human skin EST 380
C 419	8.4	49.4	12	1	ABH69839	Oligonucleotide pr	492	7.8	45.9	11	1	ABV69906	Human skin EST 769
420	8.4	49.4	12	1	ABI21482	Oligonucleotide pr	493	7.8	45.9	11	1	ABV70411	Human skin EST 819
C 421	8.4	49.4	12	1	ABH78310	Oligonucleotide pr	494	7.8	45.9	11	1	ABV62485	Human skin EST 271
C 422	8.4	49.4	12	1	ABI28957	Oligonucleotide pr	495	7.8	45.9	11	1	ABV62990	Human skin EST 776
C 423	8.4	49.4	12	1	ABI36589	Oligonucleotide pr	c 496	7.8	45.9	11	1	ABV64563	Human skin EST 234
424	8.4	49.4	12	1	ABI38671	Oligonucleotide pr	c 497	7.8	45.9	11	1	ABV62390	Human skin EST 176
425	8.4	49.4	12	1	ABI68149	Oligonucleotide pr	c 498	7.8	45.9	11	1	ABV68442	Human skin EST 622
426	8.4	49.4	12	1	ABI76866	Oligonucleotide pr	499	7.8	45.9	11	1	ABV70691	Human skin EST 847
C 427	8.4	49.4	12	1	ABH95121	Oligonucleotide pr	500	7.8	45.9	11	1	ABV63270	Human skin EST 105
C 428	8.4	49.4	12	1	ABH70717	Oligonucleotide pr	c 501	7.8	45.9	11	1	ABV65285	Human skin EST 307
C 429	8.4	49.4	12	1	ABI36041	Oligonucleotide pr	c 502	7.8	45.9	11	1	ABV71984	Human skin EST 977
C 430	8.4	49.4	12	1	ABI38817	Oligonucleotide pr	c 503	7.8	45.9	11	1	ABV71546	Human skin EST 933
C 431	8.4	49.4	12	1	ABI16173	Oligonucleotide pr	c 504	7.8	45.9	11	1	ABV64125	Human skin EST 191
C 432	8.4	49.4	12	1	ABH91205	Oligonucleotide pr	505	7.8	45.9	11	1	ABV68490	Human skin EST 627
433	8.4	49.4	12	1	ABI44592	Oligonucleotide pr	c 506	7.8	45.9	11	1	ABV69811	Human skin EST 759
434	8.4	49.4	12	1	ABI61247	Oligonucleotide pr	c 507	7.8	45.9	11	1	ADQ29773	Rat VR1 exon la tr
C 435	8.4	49.4	12	1	ABI75722	Oligonucleotide pr	c 508	7.8	45.9	11	1	ADQ35874	Human hair-bearing
C 436	8.4	49.4	12	1	ABI76793	Oligonucleotide pr	c 509	7.8	45.9	11	1	ADQ36404	Human hair-bearing
C 437	8.4	49.4	12	1	ABI18065	Oligonucleotide pr	510	7.8	45.9	11	1	ADQ33259	Human facial skin-
C 438	8.4	49.4	12	1	ABI22651	Oligonucleotide pr	c 511	7.8	45.9	11	1	ADQ32561	Human facial skin-
C 439	8.4	49.4	12	1	ABH74400	Oligonucleotide pr	c 512	7.8	45.9	11	1	ADQ33791	Human facial skin-
440	8.4	49.4	12	1	ABH99939	Oligonucleotide pr	c 513	7.8	45.9	11	1	ADQ32382	Human facial skin-
441	8.4	49.4	12	1	ABI76541	Oligonucleotide pr							
C 442	8.4	49.4	12	1	ABI04203	Oligonucleotide pr							
C 443	8.4	49.4	12	1	ABI05195	Oligonucleotide pr							
C 444	8.4	49.4	12	1	ABI08517	Oligonucleotide pr							
C 445	8.4	49.4	12	1	ABH85347	Oligonucleotide pr							
C 446	8.4	49.4	12	1	ABI50743	Oligonucleotide pr							
447	8.4	49.4	12	1	ABI79869	Oligonucleotide pr							
448	8.4	49.4	12	1	ABS65874	Inhibitory oligonu							
449	8.4	49.4	12	1	ADP78583	Chromosomal abnorm							
450	8.4	49.4	12	1	ADR98159	Human chromosome 2							
451	8.4	49.4	12	1	ADS08846	Human DNA PCR prim							
C 452	8	47.1	9	1	ABQ72166	Zinc finger protei							
C 453	8	47.1	9	1	ABQ72165	Zinc finger protei							
C 454	8	47.1	9	1	ADA64492	Zinc finger target							
C 455	8	47.1	9	1	ADA64493	Zinc finger target							
C 456	8	47.1	9	1	ADM23185	Synthetic zinc fin							
C 457	8	47.1	9	1	ADM23184	Synthetic zinc fin							
458	8	47.1	10	1	AAZ77970	Human dendritic ce							
C 459	8	47.1	10	1	AAZ77979	Human dendritic ce							
460	8	47.1	10	1	AAZ77719	Human dendritic ce							
461	8	47.1	10	1	AAZ79289	Human dendritic ce							
C 462	8	47.1	10	1	AAZ84195	Metastatic breast							
463	8	47.1	10	1	AAH63313	Human keratinocyte							
464	8	47.1	10	1	AAF34623	Yeast NORF gene SA							
465	8	47.1	10	1	AAF33976	Yeast NORF gene SA							
466	8	47.1	10	1	AAF35615	Yeast NORF gene SA							
467	8	47.1	10	1	AAF41358	Yeast NORF gene SA							
C 468	8	47.1	10	1	AAF42339	Yeast NORF gene SA							
469	8	47.1	10	1	AAF39135	Yeast NORF gene SA							
C 470	8	47.1	10	1	AAF35208	Yeast NORF gene SA							
C 471	8	47.1	10	1	AAF36519	Yeast NORF gene SA							

## ALIGNMENTS

RESULT 1  
AAT89947 standard; DNA; 17 BP.

XX AAT89947;  
XX 05-MAR-1998 (first entry)  
DT Human Interleukin-1 receptor antagonist intron 2 PCR primer 1.  
XX Interleukin-1 receptor antagonist; IL-1ra; ulcerative colitis; diagnosis;  
XX prognosis; inflammatory bowel disease; PCR primer; ss.  
OS Synthetic.  
OS Homo sapiens.  
XX WO9725445-A1.  
XX 17-JUL-1997.  
XX 08-JAN-1997; 97WO-US000042.  
XX 12-JAN-1996; 96US-00587911.  
XX (CEDA-) CEDARS SINAI MEDICAL CENT.  
PA (UYVI-) UNIV VIRGINIA PATENT FOUND.

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XX Cominelli F, Pizarro T, Rotter JI, Yang H;
PI WPI; 1997-372880/34.
DR Screening for ulcerative colitis in subjects of Jewish ancestry - by
PT detecting allele 2 of the VNTR (variable number of tandem repeats)
PT polymorphism at intron 2 of the IL-1 receptor antagonist gene.
XX Claim 7; Page 17; 22pp; English.
XX This PCR primer and primer AAT89948 are used to amplify intron 2 of the
CC human interleukin-1 receptor antagonist gene (IL-1ra) in a novel method
CC to screen for ulcerative colitis (UC) in a subject of Jewish ancestry.
CC There is an association between allele 2 of the variable number of tandem
CC repeats (VNTR) polymorphism at intron 2 of IL-1ra, an important
CC endogenous regulator of inflammation, and UC in humans of Jewish
CC ancestry. This method can be used for the diagnosis and prognosis of UC
CC in Jewish patients for UC and distinguishing UC from Crohn's disease (CD)
CC and other inflammatory disease of the bowel
XX Sequence 17 BP; 5 A; 7 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCAGCAACACTCTCTAT 17
Db 1 CTCAGCAACACTCTCTAT 17

RESULT 2
AAT89409
ID AAT89409 standard; cDNA; 17 BP.
AC AAT89409;
XX 22-APR-1998 (first entry)
DT Human IL-1RN gene intron 2 PCR primer 1.
DE Osteoporosis; interleukin-1 receptor antagonist; IL-1RN; allele;
KW bone mineral density; post-menopause; PCR primer; ss.
XX Synthetic.
OS Homo sapiens.
XX WO9738135-A1.
PN 16-OCT-1997.
PD 03-APR-1997; 97WO-US005626.
PF 05-APR-1996; 96US-00628282.
XX (MEDI-) MEDICAL SCI SYSTEMS INC.
PA Duff GW, Russell G, Eastell R;
PI WPI; 1997-512741/47.
DR Detecting genetic predisposition for osteoporosis - by detecting
XX interleukin-1 receptor antagonist gene IL-1RN allele 2 in the genomic DNA
PT of a patient.
PT Claim 2; Page 9; 21pp; English.
XX PCR primers AAT89409 and AAT89410 are used to amplify a region of the
CC interleukin-1 receptor antagonist gene, IL-1RN, intron 2 which contains a
CC variable number tandem repeat (VNTR) region that gives rise to five
CC alleles. This product is used for predicting the risk of osteoporosis in
CC a subject by determining the allelic and genetic polymorphism pattern for

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CC IL-1RN in genomic DNA. A pattern of at least one copy of the IL-1RN
CC allele 2 indicates an increased susceptibility to osteoporosis. The
CC methods can predict low bone mineral density (BMD) and the rate of bone
CC density loss and thereby a susceptibility to osteoporosis. Individuals so
CC identified can then be treated more aggressively to prevent or retard the
CC occurrence of disease
XX Sequence 17 BP; 5 A; 7 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCAGCAACACTCTCTAT 17
Db 1 CTCAGCAACACTCTCTAT 17

RESULT 3
AAV62390
ID AAV62390 standard; DNA; 17 BP.
XX AAV62390;
AC AAV62390;
XX 19-JAN-1999 (first entry)
DT IL-1 receptor antagonist gene intron 2 PCR primer #1.
DE Human; interleukin-1 receptor antagonist gene; IL-1; polymorphism;
KW diagnosis; osteoporosis; PCR primer; ss.
XX Synthetic.
OS Homo sapiens.
XX WO9844150-A1.
PN 08-OCT-1998.
PD 27-MAR-1998; 98WO-GB000944.
PF 27-MAR-1997; 97GB-00006359.
XX (GEMI-) GEMINI RES LTD.
PA Keen RW, Spector TD;
PI WPI; 1998-557135/47.
DR Diagnosis of osteoporosis by determining genotype of interleukin-1
XX receptor antagonist gene - useful for diagnosing patient pre-disposition
XX or susceptibility to osteoporosis and for therapeutic intervention.
XX Claim 9; Page 10; 36pp; English.
XX A method has been developed for the diagnosis of osteoporosis comprising
XX determining the genotype of an interleukin-1 (IL-1) receptor antagonist
XX gene (IL-1RN). The present sequence represents a PCR primer adapted to
XX amplify a portion of intron 2 of an IL-1RN for use in the method of the
XX invention. The method can be used for the diagnosis of disease, including
XX diagnosis of osteoporosis and predisposition or susceptibility to
XX osteoporosis and for therapy
XX Sequence 17 BP; 5 A; 7 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCAGCAACACTCTCTAT 17
Db 1 CTCAGCAACACTCTCTAT 17

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RESULT 4
AAV60230
ID AAV60230 standard; DNA; 17 BP.
XX AC AAV60230;
XX DT 25-NOV-1998 (first entry)
XX DE PCR primer used to amplify interleukin-1 receptor antagonist (IL-1RN).
XX KW Interleukin-1 receptor antagonist; IL-1RN; predisposition;
XX KW coronary artery disease; screen; PCR primer; ss.
XX YX Synthetic.
XX XX WO9840517-A1.
XX PD 17-SEP-1998.
XX PF 09-MAR-1998; 98WO-US004725.
XX PR 10-MAR-1997; 97US-00813456.
XX PA (MEDI-) MEDICAL SCI SYSTEMS INC.
XX PI Francis SE, Crossman DC, Duff GW;
XX DR WPI; 1998-520829/44.
XX PT Detection of predisposition to coronary artery disease - by comparative
XX PT measurement of levels of expression of alleles from the interleukin 1
XX PT locus.
XX PS Claim 6; Page 15; 22pp; English.
XX CC PCR primers AAV60230-31 were used to amplify alleles associated with the
XX CC interleukin-1 receptor antagonist (IL-1RN). The specification describes a
XX CC method for determination of a patient's predisposition to coronary artery
XX CC disease. The method comprises comparing an allele with a second allele
XX CC which is predictive of coronary artery disease, where similarity between
XX CC the first and second alleles indicates a predisposition to coronary
XX CC artery disease. The method is used to genotype an individual's
XX CC interleukin (IL)-1 loci, the overexpression of which correlates with
XX CC coronary artery disease. The method is used to screen a patients'
XX CC predisposition to coronary artery disease
XX SQ Sequence 17 BP; 5 A; 7 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCAGCAACACTCCTAT 17
Db 1 CTCAGCAACACTCCTAT 17

RESULT 5
AAV32393
ID AAV32393 standard; DNA; 17 BP.
XX AC AAV32393;
XX DT 11-SEP-1998 (first entry)
XX DE Interleukin-1RN primer 1.
XX KW Genetic polymorphism; PCR; primer; amplification; interleukin-1RN;
XX KW sight threatening diabetic retinopathy; interleukin-1-alpha; IL-1RN;
XX KW interleukin-1-beta; ss.
XX YX Synthetic.
XX OS Homo sapiens.

Query Match 100.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCAGCAACACTCCTAT 17
Db 1 CTCAGCAACACTCCTAT 17

RESULT 6
AAZ10706
ID AAZ10706 standard; DNA; 17 BP.
XX AC AAZ10706;
XX DT 23-NOV-1999 (first entry)
XX DE PCR primer 1 used to amplify part of the interleukin-1RN gene.
XX KW Polymorphism; interleukin-1RN; IL-1RN; chronic ulcer;
XX KW inflammatory cytokine; dermal ulcer; venous ulcer; pressure sore;
XX KW decubitis ulcer; PCR primer; ss.
XX YX Synthetic.
XX OS Homo sapiens.
XX KW GB2336431-A.
XX PN GB2336431-A.
XX PD 20-OCT-1999.
XX XX

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XX WO9815653-A1.
XX PD 16-APR-1998.
XX PF 09-OCT-1997; 97WO-GB002790.
XX PR 10-OCT-1996; 96GB-00021129.
XX PA (DUFF/) DUFF G.
XX PA (RENN/) RENNIE I.
XX PA (RICH/) RICHARDSON R.
XX PI Duff G, Rennie I, Richardson R;
XX DR WPI; 1998-240835/21.
XX PT Predicting increased risk of sight-threatening diabetic retinopathy -
XX PT comprises identifying genetic polymorphism pattern for genes IL-1A, IL-1B
XX PT and IL-1RN, useful to allow treatment before clinical symptoms occur.
XX PS Claim 2; Page 33; 41pp; English.
XX CC Interleukin-1RN (IL-1RN) primers 1 and 2 (AAV32394) were used to amplify
XX CC the IL-1RN gene region to identify polymorphism of the VNTR region at the
XX CC IL-1RN intron 2 locus. The invention claims to provide a method for
XX CC predicting the risk of sight threatening diabetic retinopathy. The method
XX CC involves isolating DNA from a patient and determining the DNA
XX CC polymorphism pattern of the genes that code for interleukin-1-alpha,
XX CC interleukin-1-beta and interleukin-1RN. The polymorphic pattern
XX CC identified is then compared with controls of known DNA polymorphism
XX CC patterns thereby identifying patients carrying a genetic polymorphism
XX CC associated with increased risk of sight threatening diabetic retinopathy.
XX CC The method may be able to identify diabetic patients at risk before the
XX CC clinically detectable disorders occur. Polymorphism pattern determination
XX CC of IL genes involved PCR reactions using primers AAV32389-V32398. The
XX CC method is also claimed to be useful in conjunction with identification of
XX CC other genes associated with sight threatening diabetic retinopathy in
XX CC genomic DNA and therefore, in identifying diabetic patients expressing
XX CC multiple risk patterns
XX SQ Sequence 17 BP; 5 A; 7 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCAGCAACACTCCTAT 17
Db 1 CTCAGCAACACTCCTAT 17

RESULT 6
AAZ10706
ID AAZ10706 standard; DNA; 17 BP.
XX AC AAZ10706;
XX DT 23-NOV-1999 (first entry)
XX DE PCR primer 1 used to amplify part of the interleukin-1RN gene.
XX KW Polymorphism; interleukin-1RN; IL-1RN; chronic ulcer;
XX KW inflammatory cytokine; dermal ulcer; venous ulcer; pressure sore;
XX KW decubitis ulcer; PCR primer; ss.
XX YX Synthetic.
XX OS Homo sapiens.
XX KW GB2336431-A.
XX PN GB2336431-A.
XX PD 20-OCT-1999.
XX XX

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PT useful in designing treatment strategies that modulate the activity of  
 XX proteins produced by the IL-1 gene cluster.  
 PS Claim 3; Page 33; 49pp; English.  
 XX  
 CC A method has been developed for determining a patient's susceptibility to  
 CC an inflammatory disorder. The method comprises the detection of an  
 CC interleukin 1 (IL-1) (44112332) haplotype in a sample obtained from the  
 CC patient, where its presence indicates susceptibility to an inflammatory  
 CC disorder. AAX16607 to AAX16631 represent PCR primer used in the method  
 CC for detecting the IL-1 (44112332) haplotype. The method provides kits for  
 CC the early prediction of a patient's susceptibility to inflammatory  
 CC disorders, including coronary artery disease, osteoporosis, nephropathy  
 CC in diabetes mellitus, alopecia areata, Graves disease, systemic lupus  
 CC erythematosus, lichen sclerosis and ulcerative colitis. The detection of  
 CC alleles of the haplotype can be applied to particular inflammatory  
 CC disorders, comprising diabetic retinopathy, juvenile chronic arthritis,  
 CC psoriasis, and insulin dependent diabetes. The identification of a  
 CC disease-associated haplotype enables determination of which alleles are  
 CC causative, and this information is useful in designing treatment  
 CC strategies, including gene therapy and treatment using various agents  
 CC that modulate the activity of proteins produced by the IL-1 gene cluster.  
 CC Some alleles from the IL-1 gene cluster are associated with particular  
 CC inflammatory diseases, and insufficient IL-1 production appears to act  
 CC centrally in the pathology of these diseases. Therefore, the use of IL-1  
 CC gene clusters is useful in determining genetic susceptibility to  
 CC inflammatory diseases, including those with a multifactorial etiology  
 CC with a polygenic component  
 XX  
 SQ Sequence 17 BP; 5 A; 7 C; 1 G; 4 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 17; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 15;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 CTCAGCAACACTCTCTAT 17  
 Db 1 CTCAGCAACACTCTCTAT 17  
 RESULT 9  
 ABX15549  
 ID ABX15549 standard; DNA; 17 BP.  
 XX AC ABX15549;  
 XX DT 11-APR-2003 (first entry)  
 XX DE Human IL-1 genotyping marker VNTN primer #1.  
 XX Human; ss; PCR; primer; interleukin-1; IL-1; marker VNTN; nephropathy;  
 KW inflammatory disease; Systemic Inflammatory Response; SIRS; genotyping;  
 KW Alzheimer's disease; arthritis; acute joint inflammation; ophthalmopathy;  
 KW juvenile chronic arthritis; asthma; bronchial asthma; pulmonary disease;  
 KW chronic obstructive airways disease; cardiovascular disease; thyroiditis;  
 KW atherosclerosis; autoimmune carditis; cardiomyopathy; ulcerative colitis;  
 KW cardiac cell dysfunction; aortic smooth muscle cell activation; trauma;  
 KW cardiac cell apoptosis; gastrointestinal inflammation; cerebral trauma;  
 KW inflammatory bowel disease; HIV infection; coronary artery lesion;  
 KW Kawasaki's syndrome; cervical lymphadenopathy; diabetic nephropathy;  
 KW glomerulonephritis; diabetic retinopathy; Grave's ophthalmopathy;  
 KW osteoporosis; bone loss; otitis media; pancreatitis; periodontal disease;  
 KW chronic lung disease; chronic sinusitis; chronic lymphocytic thyroiditis;  
 KW urinary tract infection; chronic prostatitis; immunological disorder;  
 KW chronic pelvic pain syndrome; alopecia areata; Grave's disease;  
 KW thyroid disease; goiter; struma lymphomatosa; sleep disorder; neoplasia;  
 KW chronic fatigue syndrome; obesity; infectious disease; leishmaniasis;  
 KW Leprosy; myocardial dysfunction; breast cancer; organ transplant;  
 KW Hodgkin's disease; hormonal regulation; fertility; septicaemia.  
 XX Homo sapiens.  
 XX US2002146700-A1.

XX 10-OCT-2002.  
 XX 27-APR-2001; 2001US-00845129.  
 XX 29-MAY-1997; 97GB-00011040.  
 XX 30-JUN-1999; 99US-00345217.  
 XX (INTE-) INTERLEUKIN GENETICS INC.  
 XX Duff GW, Cox A, Camp NJ, Di Giovine FS;  
 XX WPI; 1999-080814/07.  
 XX New method of determining a patient's susceptibility to inflammatory  
 XX disorders - by detecting the presence of an IL-1 (44112332) haplotype,  
 XX useful in designing treatment strategies that modulate the activity of  
 XX proteins produced by the IL-1 gene cluster.  
 XX Claim 5; Page 20; 42pp; English.  
 XX The invention relates to a method for determining whether a subject has  
 XX or is predisposed to developing a disease or condition that is associated  
 XX with an IL-1-inflammatory haplotype. The method involves detecting at  
 XX least one allele of the haplotype, where the presence of the allele  
 XX indicates that the subject is predisposed to the development or has the  
 XX disease or condition. The invention allows the determination of an  
 XX individual's likelihood for developing a particular disease or condition  
 XX associated with interleukin 1 (IL-1) polymorphisms without necessarily  
 XX determining or characterising the causative genetic variation. Diseases  
 XX such as inflammatory disease e.g. Systemic Inflammatory Response (SIRS),  
 XX Alzheimer's disease; arthritis e.g. acute joint inflammation, juvenile  
 XX chronic arthritis; asthma e.g. bronchial asthma, chronic obstructive  
 XX airways disease; cardiovascular diseases e.g. atherosclerosis, autoimmune  
 XX carditis; cardiomyopathy and cardiac cell dysfunction e.g. aortic smooth  
 XX muscle cell activation, cardiac cell apoptosis; gastrointestinal  
 XX inflammations e.g. inflammatory bowel disease, ulcerative colitis; HIV  
 XX infection; Kawasaki's syndrome e.g. cervical lymphadenopathy, coronary  
 XX artery lesions; nephropathies e.g. diabetic nephropathy,  
 XX glomerulonephritis; ophthalmopathies e.g. diabetic retinopathy,  
 XX ophthalmopathy; osteoporosis e.g. bone loss, otitis media; pancreatitis;  
 XX periodontal disease; pulmonary diseases e.g. chronic lung disease,  
 XX chronic sinusitis; thyroiditis e.g. chronic lymphocytic thyroiditis;  
 XX urinary tract infections e.g. chronic prostatitis, chronic pelvic pain  
 XX syndrome; immunological disorders e.g. alopecia areata, Graves disease;  
 XX thyroid diseases e.g. goiter, struma lymphomatosa; sleep disorders;  
 XX chronic fatigue syndrome; obesity; infectious diseases e.g. Leprosy,  
 XX leishmaniasis; trauma e.g. cerebral trauma, myocardial dysfunction;  
 XX neoplasias e.g. breast cancer, Hodgkin's disease; hormonal regulation e.g.  
 XX fertility, septicaemia; organ transplants. This allows for a more  
 XX customised approach to preventing the onset or progression of the disease  
 XX or condition, e.g. a clinician can more effectively prescribe a therapy  
 XX that will address the molecular basis of the disease or condition. The  
 XX present sequence represents the sequence of the human IL-1 genotyping  
 XX marker VNTN primer #1  
 XX  
 SQ Sequence 17 BP; 5 A; 7 C; 1 G; 4 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 17; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 15;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 CTCAGCAACACTCTCTAT 17  
 Db 1 CTCAGCAACACTCTCTAT 17  
 RESULT 10  
 AAZ37216  
 ID AAZ37216 standard; DNA; 17 BP.  
 XX AC AAZ37216;  
 XX



DT 28-JAN-2000 (first entry)

DE PCR primer for interleukin-1RN (VNTR).

XX PCR primer; IL-1; IL-1A; IL-1B; TNFA; interleukin-1; foetus;

KW adverse pregnancy outcome; allele detection; low birth weight; LBW;

KW pre-term baby; premature baby; tumour necrosis factor-alpha; ss.

XX Synthetic.

OS Homo sapiens.

XX WO9954707-A2.

PN 28-OCT-1999.

PD 21-APR-1999; 99WO-US008794.

PF 21-APR-1998; 98US-0082487P.

XX (MEDI-) MEDICAL SCI SYSTEMS INC.

XX Kornman KS, Offenbacher S, Duff GW;

PI WPI; 2000-013279/01.

DR Fetal testing for prediction of low birth weight by detecting an

PT interleukin allele.

XX Claim 5; Page 73; 78pp; English.

XX This sequence represents a PCR primer for interleukin-1RN (IL-1RN). The

CC invention relates to a method for determining whether a foetus is

CC predisposed to having an adverse pregnancy outcome by detecting an

CC interleukin-1A (IL-1A) (+4845) allele 2, an IL-1 (-511) allele 1 or an

CC allele in linkage disequilibrium with either of these alleles. The method

CC comprises: (a) obtaining a nucleic acid sample from the subject; and (b)

CC detecting an IL-1A (+4845) allele 2, an IL-1 (-511) allele 1 or an allele

CC in linkage disequilibrium with either of these alleles, where detection

CC of the alleles or an allele in linkage disequilibrium with them indicates

CC that the fetus is predisposed to an adverse pregnancy outcome. The method

CC is used to determine whether a fetus is predisposed to having a low birth

CC weight (LBW). By determining the IL-1 or tumour necrosis factor-alpha

CC (TNF-A) genotype an appropriate therapeutic, such as a corticosteroid,

CC antimetabolite, cytotoxic drug, colchicine or anti-cytokine, can be

CC administered to compensate for the LBW causative functional mutation. An

CC appropriate therapeutic can be used to treat a subject predisposed to

CC having a LBW baby, especially a pre-term or premature baby

XX Sequence 17 BP; 5 A; 7 C; 1 G; 4 T; 0 U; 0 Other;

SQ Query Match 100.0%; Score 17; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 15;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCAGCAACACTCCTAT 17

Db 1 CTCAGCAACACTCCTAT 17

RESULT 11

AAA61915

ID AAA61915 standard; DNA; 17 BP.

AC AAA61915;

XX 20-NOV-2000 (first entry)

DT Human IL-1RN (VNTR) polymorphic locus PCR primer, SEQ ID NO:1.

XX Human; IL-1 gene cluster; interleukin-1; chromosome 2q13-14;

KW proinflammatory; cytokine; systemic inflammatory response; sepsis;

KW dysregulation; pattern 2 allele; genotyping; IL-1RN gene;

KW IL-1 receptor antagonist; IL-1RN (VNTR) polymorphic locus;

KW variable number of tandem repeats; PCR primer; ss.

XX Homo sapiens.

XX WO200037679-A2.

XX 29-JUN-2000.

XX 01-NOV-1999; 99WO-US025633.

XX 30-OCT-1998; 98US-00183850.

XX (INTE-) INTERLEUKIN GENETICS INC.

PA Di Giovine FS, Duff GW;

PI WPI; 2000-442691/38.

DR Determining susceptibility to developing sepsis for preventing or

XX treating sepsis, involves detecting an allele of interleukin-1 genetic

PT pattern that leads to dysregulated inflammatory response.

XX Disclosure; Page 35; 66pp; English.

XX The invention relates to methods of determining an individual's

CC susceptibility to developing and/or rapidly progressing into sepsis via

CC genotyping of a member of the IL-1 (interleukin-1) gene cluster. The

CC method comprises obtaining an IL-1 gene cluster nucleic acid from an

CC individual and determining whether that individual's DNA contains at

CC least one allele of an IL-1 genetic pattern that leads to a dysregulated

CC inflammatory response. The presence of a pattern 2 allele or a marker in

CC linkage disequilibrium with a pattern 2 allele in the sample, indicates

CC that the patient has an increased susceptibility to developing sepsis.

CC The IL-1 gene cluster comprises a region of 430 kb which is located on

CC the long arm of chromosome 2 (2q13-14). It contains the IL-1A gene which

CC encodes IL-1-alpha, the IL-1B gene which encodes IL-1-beta, and the IL-

CC 1RN gene which encodes the IL-1 receptor antagonist. IL-1 is a

CC proinflammatory cytokine released by macrophages which can induce a

CC systemic response to local injury or infection. It thus plays a key role

CC in the development of sepsis, which can lead to intravascular

CC coagulation, multiple organ failure, cardiovascular collapse, and death.

CC It is therefore useful to identify those individuals who are at risk of

CC developing an exaggerated systemic inflammatory response to septic

CC stimuli, so that sepsis therapy (e.g. with IL-1 modulators) can be

CC tailored to the individual's genetic profile. Sequences AAA61915-A61928

CC represent PCR primers which may be used to amplify IL-1 gene cluster

CC polymorphic loci. Sequences AAA61915-A61916 are primers used to amplify

CC and type the IL-1RN (VNTR) (variable number of tandem repeats)

CC polymorphic locus

XX Sequence 17 BP; 5 A; 7 C; 1 G; 4 T; 0 U; 0 Other;

SQ Query Match 100.0%; Score 17; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 15;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCAGCAACACTCCTAT 17

Db 1 CTCAGCAACACTCCTAT 17

RESULT 12

AA63787

ID AAC63787 standard; DNA; 17 BP.

XX AAC63787;

XX 08-FEB-2001 (first entry)

DT Human IL-1RN gene VNTR primer #1.

XX Human; IL-1RN; interleukin-1 receptor; cytostatic; antiinflammatory;

KW immunosuppressive; dermatological; antimicrobial; antiarthritic;

KW

KW IL-1 receptor antagonist;  
 KW tumour necrosis factor alpha antagonist interstitial lung disease;  
 KW interstitial pneumonia; pulmonary fibrosis; rheumatoid arthritis;  
 KW systemic lupus erythematosus; Sjogren's syndrome; systemic sclerosis;  
 KW dermatomyositis; chromosome 2; primer; ss.  
 OS Homo sapiens.  
 XX WO2000060117-A2.  
 PN 12-OCT-2000.  
 XX 31-MAR-2000; 2000WO-US008492.  
 PF 02-APR-1999; 99US-00286108.  
 XX (INTE-) INTERLEUKIN GENETICS INC.  
 XX Duff GW, Di Giovine FS, Whyte M;  
 XX WPI; 2000-656234/63.  
 DR Method for predicting the risk of interstitial lung disease, comprising  
 XX detecting an interleukin-1 receptor antagonist allele and tumor necrosis  
 PT alpha allele or an allele in linkage disequilibrium with either of these  
 PT alleles.  
 XX Example 2; Page 72; 102pp; English.  
 PS The present sequence is provided in a specification relating to a method  
 XX for determining whether a subject has or is predisposed to develop an  
 CC interstitial lung disease. The method involves detecting an interleukin-1  
 CC receptor antagonist (IL-1RN) (+2018) allele 2, a tumour necrosis alpha  
 CC (TNF-A)(-308) allele 2, or an allele in linkage disequilibrium with  
 CC either of these two alleles. The method may be used to determine whether  
 CC a subject has or is predisposed to develop an interstitial pneumonia or a  
 CC pulmonary fibrosis and other disorders such as rheumatoid arthritis,  
 CC systemic lupus erythematosus, Sjogren's syndrome, systemic sclerosis,  
 CC dermatomyositis. The method is also used for identifying molecules which  
 CC can be used as therapeutics for treating interstitial lung disease  
 XX Sequence 17 BP; 5 A; 7 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 17; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 15;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCAGCAACACTCCTAT 17  
 |||||  
 Db 1 CTCAGCAACACTCCTAT 17

RESULT 13  
 AAF27686  
 ID AAF27686 standard; DNA; 17 BP.  
 XX AC AAF27686;  
 XX DT 02-APR-2001 (first entry)  
 XX DE Primer #19.  
 XX IL-1; interleukin; inflammation; infection; ss.  
 XX Unidentified.  
 XX WO200100880-A2.  
 PN 04-JAN-2001.  
 PD 30-JUN-2000; 2000WO-US018318.  
 PF 30-JUN-1999; 99US-00345217.  
 XX

XX (INTE-) INTERLEUKIN GENETICS INC.  
 XX Duff GW, Cox A, Camp NJ, Di Giovine FS;  
 XX WPI; 2001-102903/11.

XX Determining whether a subject has or is predisposed to disease associated  
 PT with IL-1 polymorphism involves determining presence of marker or allele  
 PT comprising IL-1 inflammatory haplotype.

XX Claim 5; Page 48; 84pp; English.

XX The present invention relates to a new method for determining whether a  
 CC subject has or is predisposed to developing a disease or condition that  
 CC is associated with an IL (interleukin)-1 inflammatory haplotype,  
 CC comprises detecting at least one allele of the haplotype, where the  
 CC presence of the allele indicates that the subject is predisposed to the  
 CC development or has the disease or condition. The method is useful for  
 CC determining whether a subject has or is predisposed to inflammatory  
 CC disease, a degenerative disease, an immunological disorder, an infectious  
 CC disease, trauma induced disease, or cancer. The above conditions  
 CC associated with an IL-1 inflammatory haplotype can be treated or  
 CC prevented by administering a therapeutic that compensates for a causative  
 CC mutation that is in linkage disequilibrium with at least one IL-1  
 CC polymorphism

XX Sequence 17 BP; 5 A; 7 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 17; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 15;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCAGCAACACTCCTAT 17  
 |||||  
 Db 1 CTCAGCAACACTCCTAT 17

RESULT 14  
 AAC89171  
 ID AAC89171 standard; DNA; 17 BP.

XX AC AAC89171;  
 XX DT 08-MAR-2001 (first entry)  
 XX Human IL-1RN (VNTR) polymorphic locus PCR primer #1.  
 DE Human; PCR primer; cardiac; vasotropic; polymorphic; chromosome 2q13;  
 XX interleukin-1 gene cluster; IL-1; cardiovascular disorder; IL-1RN;  
 KW fragile plaque disorder; occlusive disorder; in-stent restenosis; ss.

XX Homo sapiens.  
 OS WO200072015-A2.  
 XX 30-NOV-2000.  
 XX 26-MAY-2000; 2000WO-US014775.  
 XX 26-MAY-1999; 99US-00320395.  
 PR 01-NOV-1999; 99US-00431352.  
 XX (INTE-) INTERLEUKIN GENETICS INC.  
 XX Francis SE, Crossman DC, Duff GW, Kornman KS;  
 PI WPI; 2001-032066/04.  
 DR Diagnosing cardiovascular disease, or susceptibility, useful e.g. for  
 XX selecting treatment, from presence of disease-associated allele,  
 PT particularly in interleukin-1 genes.

PS Claim 11; Page 79; 121pp; English.

XX There is an association of patterns of alleles at four polymorphic loci

CC in the interleukin-1 (IL-1) gene cluster with cardiovascular disorders.

CC The present invention relates to a method for the diagnosis of a

CC cardiovascular disorder (CVD), via detecting a CVD-associated allele in a

CC patient sample. The method is used to select an appropriate therapy for

CC CVD, particularly fragile plaque disorder, occlusive disorders or in-

CC stent restenosis, or a condition associated with a mutation with linkage

CC disequilibrium with a CVD-associated allele, or to identify risk factors

CC for CVD, and to formulate a treatment designed to reduce the risk. The

CC present sequence is a PCR primer used in the present invention. The IL-1

CC gene cluster is found at the 2q13 region of chromosome 2

XX

SQ Sequence 17 BP; 5 A; 7 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 17; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 15;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCAGCAACACTCCTAT 17

Db 1 CTCAGCAACACTCCTAT 17

RESULT 15

AAC91425

ID AAC91425 standard; DNA; 17 BP.

XX

AC AAC91425;

XX

XX 20-MAR-2001 (first entry)

XX

DE Human IL-1RN (VNTR) polymorphic locus 5' PCR primer.

XX

KW Human; IL-1A; interleukin-1alpha; IL-1B; interleukin-1beta; IL-1RN;

KW interleukin-1 receptor antagonist; vasotropic; antiinflammatory;

KW hypotensive; anticoagulant; antilipaeamic; arterial restenosis;

KW restenosis associated allele; RAA; occlusive cardiovascular disorder;

KW restenosis detection; PCR primer; ss.

XX

OS Homo sapiens.

XX

XX WO200071753-A2.

PN

XX

XX 30-NOV-2000.

PD

XX

XX 24-MAY-2000; 2000WO-US014299.

PF

XX

XX 24-MAY-1999; 99US-00317674.

PR

XX

XX 01-NOV-1999; 99US-00431352.

PR

XX

PA (INTE-) INTERLEUKIN GENETICS INC.

XX

XX Korman KS, Duff GW, Crossman DC, Francis SE, Stephenson K;

PI

XX

XX WPI; 2001-025173/03.

DR

XX

PT Diagnosing or determining susceptibility to developing restenosis

PT involves detecting restenosis associated allele in a nucleic acid sample.

XX

PS Claim 5; Page 11; 129pp; English.

XX

XX The present sequence may be used in a method for determining whether a

CC subject has or is predisposed to developing an arterial restenosis. The

CC method comprises detecting a restenosis associated allele (RAA) in a

CC nucleic acid sample from the subject, where detection of the RAA

CC indicates that the subject has or is predisposed to the development of a

CC restenosis. The restenosis associated allelic pattern permits the

CC diagnosis of occlusive cardiovascular disorder. The diagnosis allows the

CC most suitable treatment methods for restenosis to be used e.g. selecting

CC therapies for initial vascular stenosis most likely to avoid subsequent

CC stenoses. The detection methods identify restenosis therapeutics,

CC

CC agonists and antagonists, (proteins, peptides, peptidomimetics, small

CC molecules or nucleic acids, e.g. anti-sense, ribozyme and triplex nucleic

CC acids) which are used to treat restenosis

XX

SQ Sequence 17 BP; 5 A; 7 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 17; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 15;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCAGCAACACTCCTAT 17

Db 1 CTCAGCAACACTCCTAT 17

RESULT 16

AAD27377

ID AAD27377 standard; DNA; 17 BP.

XX

AC AAD27377;

XX

XX 18-APR-2002 (first entry)

DT

XX

DE PCR primer #1, used for genotyping human IL-1RN (VNTR) marker.

XX

XX Human; interleukin-1; inflammatory disorder; coronary artery disease;

KW periodontal disease; Alzheimer's disease; atherosclerosis; osteoporosis;

KW immune response; insulin-dependent diabetes; diabetic retinopathy;

KW renal disease; diabetic nephropathy; hepatic fibrosis; aplasia areata;

KW Graves disease; Graves ophthalmopathy; systemic lupus erythematosus;

KW extrathyroid disease; lichen sclerosis; ulcerative colitis; asthma;

KW rheumatoid arthritis; gastric cancer; juvenile chronic arthritis;

KW interstitial lung disease; idiopathic pulmonary fibrosis; sepsis;

KW multiple sclerosis; acne; IL-1 receptor antagonist; IL-1RN; VNTR;

KW cardiant; dermatological; nootropic; neuroprotective; osteopathic;

KW ophthalmological; PCR primer; ss.

XX

OS Homo sapiens.

XX

XX WO200200933-A2.

PN

XX

XX 03-JAN-2002.

PD

XX

XX 22-JUN-2001; 2001WO-US020079.

PF

XX

XX 23-JUN-2000; 2000US-0213853P.

PR

XX

XX (INTE-) INTERLEUKIN GENETICS INC.

PA

XX

XX Duff GW, Kornman KS;

PI

XX

XX WPI; 2002-139934/18.

DR

XX

PT Screening a substance in a subject for modulating an immune response,

PT comprises genotyping to identify the test subject, and observing a

PT biomarker before and after contacting the subject with the test

PT substance.

XX

XX Example; Page 40; 54pp; English.

PS

XX

XX The present invention relates to methods for identifying a test substance

CC that modulate the immune response in a genotype specific manner. Methods

CC of the invention involve genotyping subjects to identify those having a

CC genotype (e.g. interleukin-1; IL-1) associated with one or more

CC inflammatory disorder. The method comprises genotyping a subject having

CC an inflammatory disease-associated genotype and observing a biomarker in

CC the subject before and after the subject is contacted with the test

CC substance. The methods or cells associated with inflammatory diseases are

CC useful for identifying a substance that is likely to prevent or diminish

CC a specific biological response in subjects having inflammatory disease-

CC associated genotype, where the genotype is associated a pre-disposition

CC to one or more of periodontal disease, coronary artery disease,

CC Alzheimer's disease, atherosclerosis, osteoporosis, insulin-dependent

CC diabetes, diabetic retinopathy, end-stage renal disease, diabetic  
 CC nephropathy, hepatic fibrosis, alopecia areata, Graves disease, Graves  
 CC ophthalmopathy, extrathyroid disease, systemic lupus erythematosus,  
 CC lichen sclerosus, rheumatoid arthritis, juvenile chronic arthritis,  
 CC gastric cancer, ulcerative colitis, asthma, interstitial lung disease,  
 CC multiple sclerosis, idiopathic pulmonary fibrosis, sepsis and acne. The  
 CC invention also relates to a kit comprising primers for the identification  
 CC of one or more IL-1 polymorphisms. The present sequence is a PCR primer  
 CC which is used for amplifying IL-1 receptor antagonist (IL-1RN; VNPR)  
 CC gene. This primer is used in the exemplification of the invention for  
 CC genotyping IL-1RN marker

XX Sequence 17 BP; 5 A; 7 C; 1 G; 4 T; 0 U; 0 Other;  
 SQ Query Match 100.0%; Score 17; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 15;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCAGCAACACTCCTAT 17  
 Db |||||

RESULT 17  
 AAL54501  
 ID AAL54501 standard; DNA; 17 BP.  
 XX AC AAL54501;  
 DT 16-APR-2003 (first entry)  
 XX Ageing-related condition detection PCR primer, SEQ ID No 7.  
 DE Early onset; progression; ageing-related condition; BOA; allele;  
 KW interleukin; (IL)-1; pattern 1; pattern 2; pattern 3; osteoporosis;  
 KW osteoarthritis; wrinkled skin; age-related cancer; lifestyle; exercise;  
 KW diet; nutraceutical; PCR; primer; ss.  
 XX Unidentified.  
 XX WO2002103031-A2.  
 XX 27-DEC-2002.  
 XX 17-JUN-2002; 2002WO-US019205.  
 XX 15-JUN-2001; 2001US-0298493P.  
 XX (INTE-) INTERLEUKIN GENETICS INC.  
 XX Barnett K, Crossman DC, Duff GW, Francis SE, Kornman KS;  
 PI WPI; 2003-167530/16.  
 XX Determining a subject's susceptibility to an early onset or progression  
 PT of an aging-related condition, useful for customizing therapy, comprises  
 PT detecting the presence of an allele of an interleukin-1 pattern 1,  
 PT pattern 2 and/or pattern 3.  
 XX Example 3; Page 52; 98pp; English.

XX The invention relates to a novel method for determining a subject's  
 CC susceptibility to the early onset or progression of an ageing-related  
 CC condition (EOA). The novel method comprises assessing the subject's  
 CC genotype with respect to at least one allele of an interleukin (IL)-1  
 CC pattern 1, pattern 2 and/or pattern 3 (the presence or absence of at  
 CC least 1 allele provides information about the subject's susceptibility to  
 CC an early onset or progression of an ageing-related condition). The method  
 CC is useful for determining or predicting a subject's susceptibility to the  
 CC early onset or progression of an ageing-related condition (e.g.  
 CC osteoporosis, osteoarthritis, wrinkled skin, or age-related cancer) and  
 CC for determining an ageing-related phenotype. The method may be a  
 CC customised therapy based on the individual's genetic profile, to tailor a

CC recommended lifestyle, including changes in exercise and diet, and to  
 CC recommend nutraceuticals that are predicted to benefit a subject having a  
 CC particular IL-1 genotype and BOA predisposition. This polynucleotide  
 CC sequence represents a PCR primer used in the detection method for  
 CC determining EOA predisposition of the invention

XX Sequence 17 BP; 5 A; 7 C; 1 G; 4 T; 0 U; 0 Other;  
 SQ Query Match 100.0%; Score 17; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 15;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCAGCAACACTCCTAT 17  
 Db |||||

RESULT 18  
 AAD51455  
 ID AAD51455 standard; DNA; 17 BP.  
 XX AC AAD51455;  
 DT 16-APR-2003 (first entry)  
 XX Human interleukin-1 (IL-1) gene amplifying PCR primer #7.  
 DE Drug screening; fungicide; gene therapy; antibacterial; infection;  
 KW virucide; human; interleukin-1; IL-1; PCR; primer; ss.  
 XX Homo sapiens.  
 XX WO2002101015-A2.  
 XX 19-DEC-2002.  
 XX 11-JUN-2002; 2002WO-US018346.  
 XX 11-JUN-2001; 2001US-0297305P.  
 XX (INTE-) INTERLEUKIN GENETICS INC.  
 XX Dower S, Duff GW;  
 PI WPI; 2003-148793/14.  
 XX New detection reagent, useful for monitoring molecular assembly events to  
 PT permit the dissection of genetic and non-genetic influences on biological  
 PT activity, comprises an interactive sensor pair.  
 XX Disclosure; Page 41; 56pp; English.

XX The invention relates to methods, compositions and apparatus for  
 CC monitoring molecular assembly events. It also relates to a detection  
 CC reagent comprising an interactive sensor pair. The detection reagent is  
 CC useful for monitoring molecular assembly events to permit the dissection  
 CC of genetic and non-genetic influences on a particular biological  
 CC activity. The method is useful for linking genetic variations to  
 CC molecular and physiological events, drug screening, diagnostics, therapy  
 CC selection and dosing, patient monitoring or environmental safety. The  
 CC interactive sensor pairs may be used to screen for and identify novel  
 CC agonists and antagonists or other molecules that modulate a biological  
 CC activity. The method is also useful for selecting an appropriate targeted  
 CC therapeutic for a subject having an infection, including viral, bacterial  
 CC or fungal infection. It is also used in gene therapy. The present  
 CC sequence is a PCR primer used for amplifying human interleukin-1 (IL-1)  
 CC gene. This sequence is used to illustrate the method of the invention

XX Sequence 17 BP; 5 A; 7 C; 1 G; 4 T; 0 U; 0 Other;  
 SQ Query Match 100.0%; Score 17; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 15;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



```

XX PI Duff GW, Di Giovine PS, Barnes PJ, Lim S;
XX WPI; 2004-429802/40.
XX
XX PT Determining whether a subject has or is predisposed to developing an
XX obstructive airway disease (OAD), such as asthma, detecting an OAD-
XX associated allele in a nucleic acid sample from the subject, which
XX PT indicates predisposition to OAD.
XX
XX XX Example 3; SEQ ID NO 13; 61pp; English.
XX
XX CC The invention relates to a method of determining whether a subject has,
XX or is predisposed to developing, an obstructive airway disease (OAD),
XX comprising detecting an OAD-associated allele in a nucleic acid sample
XX from the subject, where the presence of OAD-associated allele indicates
XX CC that the subject has or is predisposed to the development of OAD. The OAD
XX associated allele is selected from allele 2 of interleukin-13 (IL-13)
XX (-2581), allele 2 of IL-1B (-511), allele 2 of IL-1B (+3954), or an
XX allele in linkage disequilibrium with allele 2 of IL-1B (-511) or allele
XX 2 of IL-1B (+3954) comprising allele 4 of IL-1A (222/223), allele 4 of IL
XX -1A (g25/g26), allele 1 of IL-1A (-889), allele 1 of (+3954), allele 3 of
XX CC the gaat.p3330 marker, allele 3 of the Y31 marker, allele 2 of IL-1RN
XX (-2018), allele 2 of IL-1RN (VNTR), allele 3 of IL-1A (222/223), allele 3
XX of IL-1A (g25/g26), allele 2 of IL-1A (-889), allele 1 of IL-1B (-511),
XX allele 4 of the gaat.p3330 marker, allele 6 of the Y31 marker, allele 1
XX of IL-1RN (+2018), and allele 1 of IL-1RN (VNTR). The method is useful
XX CC for determining whether a subject has or is predisposed to developing an
XX OAD, particularly asthma. The method is especially useful for the early
XX CC identification of those who are generally susceptible to OAD, and those
XX who are susceptible to acute episodes. Early identification would
XX facilitate the prevention or administration of appropriate treatment at
XX the earliest stage, thus increasing the probability of a positive
XX CC outcome. The present sequence represents a PCR primer used to detect
XX polymorphisms in the human interleukin-1 (IL-1) gene locus.
XX
XX SQ Sequence 17 BP; 5 A; 7 C; 1 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 17; DB 1; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 15;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 CTCAGCAACACTCTCTAT 17
XX Db 1 CTCAGCAACACTCTCTAT 17
XX
XX RESULT 22
XX ADU16279
XX ID ADU16279 standard; DNA; 17 BP.
XX XX
XX AC ADU16279;
XX
XX DT 27-JAN-2005 (first entry)
XX
XX DE Human interleukin-1R genotyping primer seqid 29.
XX
XX KW seronegative spondyloarthropathy; interleukin 1; IL-1;
XX KW ankylosing spondylitis; interleukin-1R; IL-1R; PCR; primer; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO2004097045-A1.
XX
XX PD 11-NOV-2004.
XX
XX PF 04-MAY-2004; 2004WO-GB001905.
XX
XX PR 01-MAY-2003; 2003GB-00010060.
XX
XX PA (ISIS-) ISIS INNOVATION LTD.
XX
XX PI Brown MA;
XX
XX WPI; 2004-804774/79.
XX
XX PT Detecting, in vitro, whether a subject has or is genetically predisposed
XX to a seronegative spondyloarthropathy comprises determining the presence
XX of a polymorphism in interleukin 1 gene region of chromosome 2.
XX
XX XX Example; SEQ ID NO 29; 40pp; English.
XX
XX CC The invention describes a method of detecting, in vitro, whether a
XX subject has or is genetically predisposed to a seronegative
XX spondyloarthropathy comprises determining the presence of a genetic
XX polymorphism within the interleukin 1 (IL-1) gene region of chromosome 2
XX extending from IL-1A to the beginning of IL-1RN in a genetic sample
XX obtained from a subject. Also described are: an isolated polynucleotide,
XX useful for diagnosing whether a subject has or is predisposed to a
XX seronegative spondyloarthropathy, comprising at least a contiguous
XX sequence of 15 bases derived from the IL-1 gene region, or its complement
XX ; and a diagnostic kit comprising the polynucleotide. The polynucleotide
XX is useful for determining whether a subject has or is predisposed to a
XX seronegative spondyloarthropathy. The method and kit are useful for
XX CC diagnosing seronegative spondyloarthropathy, i.e. ankylosing spondylitis.
XX This sequence represents an interleukin-1R (IL-1R) primer used to
XX CC genotype the IL-1R gene.
XX
XX SQ Sequence 17 BP; 5 A; 7 C; 1 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 17; DB 1; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 15;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 CTCAGCAACACTCTCTAT 17
XX Db 1 CTCAGCAACACTCTCTAT 17
XX
XX RESULT 23
XX ADU48041
XX ID ADU48041 standard; DNA; 17 BP.
XX XX
XX AC ADU48041;
XX
XX DT 10-FEB-2005 (first entry)
XX
XX DE Human IL-1A (VNTR) polymorphic locus amplifying PCR primer #1.
XX
XX KW Restenosis; interleukin; IL; IL-1A; IL-1B; IL-1RN; vasotropic; human;
XX KW PCR; primer; ss.
XX
XX OS Homo sapiens.
XX
XX PN US2004229264-A1.
XX
XX PD 18-NOV-2004.
XX
XX PF 12-APR-2004; 2004US-00823197.
XX
XX PR 10-MAR-1997; 97US-00813456.
XX PR 26-MAY-1999; 99US-00320395.
XX PR 01-NOV-1999; 99US-00431352.
XX PR 24-MAY-2000; 2000US-00578534.
XX
XX PA (INTE-) INTERLEUKIN GENETICS INC.
XX
XX PI Crossman DC, Duff GW, Francis SE, Kornman KS, Stephenson K;
XX
XX WPI; 2004-813241/80.
XX
XX PT New kit comprises a first primer oligonucleotide that hybridizes 5' or 3'
XX to an allele 1 of IL-1A (+4845), IL-1B (-511), IL-1B (+3954), IL-1RN
XX (VNTR), or IL-1RN (+2018), useful for diagnosing, treating, or preventing
XX restenosis.
XX

```

PS Claim 11; SEQ ID NO 7; 81bp; English.

XX The invention relates to a kit for determining the existence of or a

CC susceptibility to developing a restenosis in a subject. The kit comprises

CC of a primer that hybridizes 5' or 3' to an allele selected from allele 1

CC of the following markers, interleukin (IL)-1A (+4845), IL-1B (-511), IL-

CC 1B (+3954), IL-1RN (VNTR) or IL-1RN (+2018) or an allele in linkage

CC disequilibrium with it. The kit is useful for determining the existence

CC of or a susceptibility to developing a restenosis in a subject. It is

CC also useful for determining whether a subject has or is predisposed to

CC developing restenosis or for treating or preventing restenosis. The

CC present sequence is a PCR primer used for amplifying human IL-1A gene

CC polymorphic locus.

XX

SQ Sequence 17 BP; 5 A; 7 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 17; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 15;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCAGCAACACTCCTAT 17

Db 1 CTCAGCAACACTCCTAT 17

RESULT 24

ADY72754

ID ADY72754 standard; DNA; 17 BP.

XX

AC ADY72754;

XX

DT 02-JUN-2005 (first entry)

DE Human IL-1RN PCR primer SEQ ID NO:5.

XX interleukin-1 receptor; menopause; gynecological; obstetrics;

KW metabolic disorder; PCR; primer; ss.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN US2005064453-A1.

XX

PD 24-MAR-2005.

XX

PF 03-MAY-2004; 2004US-00838503.

XX

PR 30-JUN-1999; 99US-00345217.

PR 04-AUG-2000; 2000US-00632657.

XX

PA (DUFF/) DUFF G.

PA (KORN/) KORNMAN K.

PA (DIJK/) DIJK S V.

XX

PI Duff G, Kornman K, Dijk SV;

XX

DR WPI; 2005-241272/25.

XX

PT New kit for determining a woman's predisposition to early-onset menopause

PT (EOM) comprises primers that hybridize to a marker of an IL-1-related

PT gene associated with EOM, a DNA sampling means, a control, and a DNA

PT detection means.

XX

PS Claim 5; SEQ ID NO 5; 59pp; English.

XX

CC The invention relates to a kit for determining a woman's predisposition

CC to early-onset menopause (EOM). The kit comprises a first primer that

CC hybridizes 5' or 3' to a marker of an IL-1-related gene associated with

CC early-onset menopause. Gynecological. The kit is useful for detecting a

CC predisposition to EOM, for treating or preventing the development of EOM

CC in a woman, or for identifying agents that may treat or prevent EOM. The

CC present sequence represents a PCR primer for the human interleukin 1

CC receptor antagonist (IL-1RN) gene, which is used in an example from the

CC

CC present invention for determining an individuals allelic pattern

CC (genotyping). The human IL-1RN gene is located on chromosome 2, more

CC specifically to q13-14.1. Note: the present sequence is designated SEQ ID

CC NO:5 in the examples and claims, but corresponds with SEQ ID NO:9 in the

CC Sequence Listing.

XX

SQ Sequence 17 BP; 5 A; 7 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 17; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 15;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCAGCAACACTCCTAT 17

Db 1 CTCAGCAACACTCCTAT 17

RESULT 25

AEE01079

ID AEE01079 standard; DNA; 17 BP.

XX

AC AEE01079;

XX

DT 26-JAN-2006 (first entry)

DE Human interleukin (IL)-1 PCR primer SEQ ID NO 22.

XX

KW periodontal disease; interleukin; IL-1; PCR; primer; ss.

XX

OS Homo sapiens.

PN WO2005108619-A2.

XX

PD 17-NOV-2005.

XX

PF 03-MAY-2005; 2005WO-US015267.

XX

PR 03-MAY-2004; 2004US-0567727P.

XX

PA (INTE-) INTERLEUKIN GENETICS INC.

XX

PI Duff GW, Kornman K, Wilkins L, Chen HM, Rogus J;

XX

DR WPI; 2005-811015/82.

XX

PT Identifying a subject having increased IL-1B transcription, for

PT identifying if the subject is predisposed to periodontal disease, by

PT providing a biological sample comprising genomic DNA, and identifying an

PT IL-1B allele in the sample.

XX

PS Example 1; SEQ ID NO 22; 126pp; English.

XX

CC The invention relates to a method of identifying a subject having

CC increased IL-1B transcription providing a biological sample comprising

CC genomic DNA from the subject, and identifying an IL-1B allele selected

CC from IL-1B (-3737) allele 1 and/or IL-1B (-1468) allele 1 in the sample,

CC where the presence of the allele indicates that the subject has increased

CC IL-1B transcription. The methods are useful for identifying if the

CC subject is predisposed to periodontal disease, and as assays for

CC identifying therapeutics for treating and/or preventing the development

CC of the disease. The present sequence represents a human interleukin (IL)-

CC 1 PCR primer.

XX

SQ Sequence 17 BP; 5 A; 7 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 17; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 15;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCAGCAACACTCCTAT 17

Db 1 CTCAGCAACACTCCTAT 17

```

RESULT 26
ID ACC44794 standard; DNA; 17 BP.
XX
AC ACC44794;
XX
DT 03-JUN-2003 (first entry)
XX
DE Interleukin 1 beta PCR primer SEQ ID NO:5.
XX
KW Interleukin 1 beta; IL-1 beta; hepatitis C virus; HCV; infection;
XX liver cancer; cytostatic; PCR primer; ss.
XX
OS Homo sapiens.
XX Synthetic.
XX
PN WO2003016570-A1.
XX
PD 27-FEB-2003.
XX
PF 21-AUG-2002; 2002WO-JP008415.
XX
PR 21-AUG-2001; 2001JP-00250545.
XX
PA (HUBI-) HUBIT GENOMIX INC.
XX
PI Omata M, Kato N;
XX
DR WPI; 2003-256715/25.
XX
PT Examining liver cell cancer particularly after infection with hepatitis
PT virus by using polymorphism of IL-1beta gene, also applicable in
PT screening preventives or remedies for liver cell cancer.
XX
PS Example 2; Page 33; 55pp; Japanese.
XX
CC The present invention describes a method for examining liver cell cancer
CC caused by hepatitis virus, where the method comprises the detection of a
CC polymorphism produced at the promoter region of interleukin 1 (IL-1) beta
CC gene. IL-1 beta has cytostatic activity. The method is for examining
CC liver cell cancer particularly after infection with hepatitis C virus
CC (HCV), which can also be applied in screening drugs for the prevention or
CC treatment of liver cell cancer. The present sequence represents a PCR
CC primer for IL-1 beta, which is used in an example from the present
CC invention
XX
SQ Sequence 17 BP; 4 A; 10 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 82.4%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCAGCAACTCC 14
Db 4 CTCAGCAACTCC 17

RESULT 27
ADU50588
ID ADU50588 standard; DNA; 17 BP.
XX
AC ADU50588;
XX
DT 10-FEB-2005 (first entry)
XX
DE IL-1RN VNTR polymorphism PCR primer, SEQ ID 9.
XX
KW Immunosuppressive; Gene Therapy; kidney; interleukin-1; PCR; primer; ss.
XX Synthetic.
XX
PN US2004229228-A1.
XX

Query Match 82.4%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCAGCAACTCC 14
Db 4 CTCAGCAACTCC 17

RESULT 28
AAD48159/c
ID AAD48159 standard; DNA; 16 BP.
XX
AC AAD48159;
XX
DT 24-FEB-2003 (first entry)
XX
DE PCR primer #7 used for single nucleotide polymorphism (SNP) analysis.
XX
KW Peptide nucleic acid; PNA; nucleic acid zygosity; genetic analysis;
XX scientific investigation; pharmacogenomic; pharmacogenetic; epigenomic;
XX PCR; primer; ss.
XX
OS Unidentified.
XX
PN WO200272865-A2.
XX
PD 19-SEP-2002.
XX
PF 09-MAR-2002; 2002WO-US007050.
XX
PR 09-MAR-2001; 2001US-0274547P.
XX
PA (BOST-) BOSTON PROBES INC.
XX
PI Coull JM, Flandaca MJ, Kristjanson MD, Hyldig-Nielsen JJ;
XX Creasey TM;
XX WPI; 2003-018741/01.
XX

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XX
PD 18-NOV-2004.
XX
PF 24-JUL-2003; 2003US-00626830.
XX
PR 25-JUL-2002; 2002US-0398986P.
XX
PA (NOUN ) UNIV NORTHWESTERN.
XX (AMGE-) AMGEN INC.
XX
PI Sims JE, Kaufman DB;
XX WPI; 2005-010687/01.
XX
PT Diagnosing early kidney allograft rejection comprises determining a
PT genotype of an IL-1 family member gene.
XX
PS Example 1; SEQ ID NO 9; 12pp; English.
XX
CC The present invention relates to a method for identifying an individual
CC predisposed to early rejection of a kidney allograft. The method
CC comprises determining a genotype of an interleukin-1 (IL-1) family member
CC gene, where the presence of one or more alleles, e.g. an A1, A2 allele
CC combination at an IL-1A VNTR intron 6 locus, an A2 allele at an IL-
CC 1A-4845 locus, or an E2 allele at an IL-1B-3953 locus indicates that the
CC individual is at increased risk for early rejection of the kidney
CC allograft. Also claimed is a primer set for determining a genotype in an
CC IL-1 family member gene. The present sequence is one such primer. The
CC methods and primers are useful for identifying an individual predisposed
CC to and treating a patient predisposed to early rejection of a kidney
CC allograft.
XX
SQ Sequence 17 BP; 4 A; 10 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 82.4%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCAGCAACTCC 14
Db 4 CTCAGCAACTCC 17

RESULT 28
AAD48159/c
ID AAD48159 standard; DNA; 16 BP.
XX
AC AAD48159;
XX
DT 24-FEB-2003 (first entry)
XX
DE PCR primer #7 used for single nucleotide polymorphism (SNP) analysis.
XX
KW Peptide nucleic acid; PNA; nucleic acid zygosity; genetic analysis;
XX scientific investigation; pharmacogenomic; pharmacogenetic; epigenomic;
XX PCR; primer; ss.
XX
OS Unidentified.
XX
PN WO200272865-A2.
XX
PD 19-SEP-2002.
XX
PF 09-MAR-2002; 2002WO-US007050.
XX
PR 09-MAR-2001; 2001US-0274547P.
XX
PA (BOST-) BOSTON PROBES INC.
XX
PI Coull JM, Flandaca MJ, Kristjanson MD, Hyldig-Nielsen JJ;
XX Creasey TM;
XX WPI; 2003-018741/01.
XX

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XX Composition for determining target sequence of contiguous nucleobases.  
 PT comprises polynucleobase strand and combination oligomer comprising first  
 PT and second oligomer blocks that are covalently linked to each other.  
 XX  
 XX Example 5; Page 70; 149pp; English.  
 XX  
 CC The present invention relates to combination oligomers, including block  
 CC synthesis of combination of oligomers in the absence of a template. The  
 CC invention relates to a composition comprising a polynucleobase strand and  
 CC a combination oligomer comprising first and second oligomer blocks that  
 CC are each independently a peptide nucleic acid (PNA) covalently linked to  
 CC each other by a linker of at least three atoms in length, where the  
 CC oligomer blocks are sequences specifically hybridised to a target  
 CC sequence of contiguous nucleobases in the polynucleobase strand. To form  
 CC a double stranded target sequence-oligomer complex. The composition is  
 CC used for determining a target sequence of contiguous nucleobases and for  
 CC determining the zygosity of a nucleic acid for a single nucleotide  
 CC polymorphism (SNP). The methods are useful in scientific investigation,  
 CC e.g., for detection, identification and/or enumeration of bacteria,  
 CC viruses and pathogens in food, beverages, water, pharmaceutical products,  
 CC personal care products, dairy products, in clinical samples or in samples  
 CC of plant, animal, human or environmental origin. They are also useful for  
 CC the analysis of raw materials, equipment, products or processes used to  
 CC manufacture or store food, beverages, water, pharmaceutical products,  
 CC personal care products dairy products or environmental samples. The  
 CC methods and materials are useful in areas such as expression analysis,  
 CC SNP analysis, genetic analysis of humans, animals, fungi, yeast viruses  
 CC and plants, therapy monitoring, pharmacogenomics, pharmacogenetics,  
 CC epigenomics and high throughput screening operations. The present  
 CC sequence is a PCR primer used for single nucleotide polymorphism (SNP)  
 CC analysis  
 XX

Sequence 16 BP; 3 A; 1 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 72.9%; Score 12.4; DB 1; Length 16;  
 Best Local Similarity 92.9%; Pred. No. 68;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TCAGCACCACTCTCT 15  
 Db 15 TCAGCACCACTCTCT 2

## RESULT 29

ID ACN01682  
 ACN01682 standard; RNA; 17 BP.

XX ACN01682;

XX 22-APR-2004 (first entry)

XX WNV Inozyme substrate SEQ ID NO 1672.

XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;  
 KW viricide; neuroprotective; antibacterial; replication; pancreatitis;  
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;  
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;  
 KW Amberzyme; Zinzyne; ss.

XX West Nile Virus.

XX WO200268637-A2.

XX 06-SEP-2002.

XX 19-OCT-2001; 2001WO-US048350.

XX 20-OCT-2000; 2000US-0242411P.

XX (RIBO-) RIBOZYME PHARM INC.

XX (BLAT/) BLATT L.

XX (MCSW/) MCSWIGGEN J A.

XX Blatt L, Mcswiggen JA;  
 PI WPI; 2002-706994/76.  
 DR  
 XX New nucleic acid molecule that modulates replication of West Nile Virus  
 PT (WNV), useful for treating a condition related to WNV infection e.g.  
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.  
 XX  
 XX Claim 23; SEQ ID NO 1672; 495pp; English.

XX The invention relates to nucleic acid molecules that modulate replication  
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for  
 CC treating a condition related to WNV infection e.g. pancreatitis,  
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
 CC molecule is selected from the group of ribozymes consisting of  
 CC Hammerhead, inozyme, G-cleaver, DNAzyme, Amberzyme and zinzyne. The  
 CC nucleic acid molecules further comprise at least five ribose residues, at  
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at  
 CC least three of the 5' terminal nucleotides and a 3' end modification of a  
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
 CC in the specification. The present sequence is that of a nucleic acid  
 CC molecule of the invention

XX Sequence 17 BP; 4 A; 6 C; 2 G; 0 T; 5 U; 0 Other;

Query Match 72.9%; Score 12.4; DB 1; Length 17;  
 Best Local Similarity 71.4%; Pred. No. 74;  
 Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 TCAGCACCACTCTCT 15  
 Db 4 UCAGCAUCACUCCU 17

## RESULT 30

ID ACN01683  
 ACN01683 standard; RNA; 17 BP.

XX ACN01683;

XX 22-APR-2004 (first entry)

XX WNV Inozyme substrate SEQ ID NO 1673.

XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;  
 KW viricide; neuroprotective; antibacterial; replication; pancreatitis;  
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;  
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;  
 KW Amberzyme; Zinzyne; ss.

XX West Nile Virus.

XX WO200268637-A2.

XX 06-SEP-2002.

XX 19-OCT-2001; 2001WO-US048350.

XX 20-OCT-2000; 2000US-0242411P.

XX (RIBO-) RIBOZYME PHARM INC.

XX (BLAT/) BLATT L.

XX (MCSW/) MCSWIGGEN J A.

XX Blatt L, Mcswiggen JA;

XX WPI; 2002-706994/76.

XX New nucleic acid molecule that modulates replication of West Nile Virus  
 PT (WNV), useful for treating a condition related to WNV infection e.g.

•

CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
 CC in the specification. The present sequence is that of a nucleic acid  
 CC molecule of the invention

XX Sequence 17 BP; 5 A; 2 C; 6 G; 0 T; 4 U; 0 Other;

Query Match 72.9%; Score 12.4; DB 1; Length 17;  
 Best Local Similarity 92.9%; Pred. No. 74;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TCAGCAACACTCTCT 15  
 Db 15 TCAGCATCACTCTCT 2

RESULT 33  
 ACN15151/c  
 ID ACN15151 standard, RNA; 17 BP.

XX ACN15151;

AC ACN15151;

DT 22-APR-2004 (first entry)

DE WNV minus strand Amberzyme substrate SEQ ID NO 15154.

XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;  
 KW viricide; neuroprotective; antibacterial; replication; pancreatitis;  
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;  
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;  
 KW Amberzyme; Zinzyme; ss.

XX West Nile Virus.

OS WO200268637-A2.

PN 06-SEP-2002.

PD 19-OCT-2001; 2001WO-US048350.

PF 20-OCT-2000; 2000US-0242411P.

PR (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

PA (MCSW/) MCSWIGGEN J A.

XX Blatt L, Mcswiggen JA;

XX WPI; 2002-706994/76.

XX New nucleic acid molecule that modulates replication of West Nile Virus  
 PT (WNV), useful for treating a condition related to WNV infection e.g.  
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

XX Claim 23; SEQ ID NO 15154; 495pp; English.

XX The invention relates to nucleic acid molecules that modulate replication  
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for  
 CC treating a condition related to WNV infection e.g. pancreatitis,  
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
 CC molecule is selected from the group of ribozymes consisting of  
 CC Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyme. The  
 CC nucleic acid molecules further comprise at least five ribose residues, at  
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at  
 CC least three of the 5' terminal nucleotides and a 3' end modification of a  
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
 CC in the specification. The present sequence is that of a nucleic acid  
 CC molecule of the invention

XX Sequence 17 BP; 5 A; 2 C; 7 G; 0 T; 3 U; 0 Other;

Query Match 72.9%; Score 12.4; DB 1; Length 17;  
 Best Local Similarity 92.9%; Pred. No. 74;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TCAGCAACACTCTCT 15  
 Db 16 TCAGCATCACTCTCT 3

RESULT 34  
 ABI02395/c  
 ID ABI02395 standard; DNA; 12 BP.

XX ABI02395;

AC ABI02395;

DT 22-FEB-2002 (first entry)

XX Oligonucleotide primer SEQ ID NO 302368 for detecting SNP TSC0019966.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

OS WO200177384-A2.

PN 18-OCT-2001.

PD 06-APR-2001; 2001WO-IB000713.

PF 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.

XX Claim 1; SEQ ID NO 302368; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC9989, ABF0010-ABF9989, ABH0010-ABH9989 and ABI0010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 12 BP; 3 A; 0 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 64.7%; Score 11; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 76;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CAACACTCTCTA 16  
 Db 11 CAACACTCTCTA 1

RESULT 35  
 ABK72568  
 ID ABK72568 standard; DNA; 12 BP.

XX

AC ABK72568;  
 XX 13-AUG-2002 (first entry)  
 DT Human OPAL gene, exon/intron junction #35.  
 XX Human, ophthalmological; OPAL; autosomal dominant optic atrophy; ADOA;  
 DE gene; ds.  
 XX Homo sapiens.  
 OS WO200227022-A2.  
 XX 04-APR-2002.  
 XX 26-SEP-2001; 2001WO-GB004284.  
 XX 26-SEP-2000; 2000GB-00023555.  
 XX (UNLO) UNIV COLLEGE LONDON.  
 PA (UYEY-) UNIV EYE HOSPITAL.  
 XX Bhattacharya S, Wisinger B, Alexander C, Votruba M;  
 PI WPI; 2002-416484/44.  
 XX Novel human normal or mutant OPAL (the predominant locus for autosomal  
 XX dominant optic atrophy (ADOA)) polypeptides and the OPAL gene, useful in  
 PT the diagnosis and treatment of autosomal dominant optic atrophy ADOA.  
 PT the diagnosis and treatment of autosomal dominant optic atrophy ADOA.  
 XX Disclosure; Fig 12; 75pp; English.  
 XX The invention relates to an isolated human normal or mutant OPAL (the  
 CC predominant locus for autosomal dominant optic atrophy (ADOA))  
 CC polypeptide (I), characterised by a molecular weight of about 112 kDa,  
 CC and substantially free of other human proteins. Also described is the DNA  
 CC (ii) encoding (i), (i) and (ii) are useful as a medicament, for the  
 CC treatment of a medical condition resulting from a defect in the OPAL  
 CC gene, which results in autosomal dominant optic atrophy. The nucleic acid  
 CC and antibodies to (i) are useful in a variety of hybridisation and  
 CC immunological assays to screen for, and to detect the presence of, either  
 CC a normal or a defective OPAL gene or gene product. ABK72533-ABK72593  
 CC represent the human OPAL gene and intron/exon splice junctions  
 XX Sequence 12 BP; 4 A; 6 C; 1 G; 1 T; 0 U; 0 Other;  
 SQ Query Match 64.7%; Score 11; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 76;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 CTCAGCAACAC 11  
 Db 2 CTCAGCAACAC 12  
 |||||  
 RESULT 36  
 ABF36021  
 ID ABF36021 standard; DNA; 13 BP.  
 XX AC ABF36021;  
 XX 21-FEB-2002 (first entry)  
 DT Oligonucleotide SEQ ID NO 136018 for detecting SNP TSC0033969.  
 DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX Homo sapiens.  
 OS WO200177384-A2.  
 PN Set of oligonucleotides, useful for diagnosis and cell typing, is

PD 18-OCT-2001.  
 XX 06-APR-2001; 2001WO-IB000713.  
 XX 07-APR-2000; 2000DE-01019173.  
 PR (EPIG-) EPIGENOMICS AG.  
 PA Olek A, Piepenbrock C, Berlin K;  
 PI WPI; 2001-657177/75.  
 DR Set of oligonucleotides, useful for diagnosis and cell typing, is  
 XX designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 PT Claim 1; SEQ ID NO 136018; 29pp + Sequence Listing; German.  
 PS This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX Sequence 13 BP; 6 A; 4 C; 0 G; 3 T; 0 U; 0 Other;  
 SQ Query Match 64.7%; Score 11; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 84;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 7 AACACTCCTAT 17  
 Db 2 AACACTCCTAT 12  
 |||||  
 RESULT 37  
 ABC71077  
 ID ABC71077 standard; DNA; 13 BP.  
 XX AC ABC71077;  
 XX 21-FEB-2002 (first entry)  
 DT Oligonucleotide SEQ ID NO 71094 for detecting SNP TSC0018437.  
 DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX Homo sapiens.  
 OS WO200177384-A2.  
 PN 18-OCT-2001.  
 PD 06-APR-2001; 2001WO-IB000713.  
 XX 07-APR-2000; 2000DE-01019173.  
 PR (EPIG-) EPIGENOMICS AG.  
 PA Olek A, Piepenbrock C, Berlin K;  
 PI WPI; 2001-657177/75.  
 DR Set of oligonucleotides, useful for diagnosis and cell typing, is

PT designed to detect single-nucleotide polymorphisms and cytosine  
 XX methylation status.  
 XX  
 PS Claim 1; SEQ ID NO 71094; 29pp + Sequence Listing; German.  
 XX  
 CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 13 BP; 4 A; 6 C; 0 G; 3 T; 0 U; 0 Other;  
 Query Match 64.7%; Score 11; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 84;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 6 CAACACTCCTA 16  
 Db 1 CAACACTCCTA 11  
 |||||  
 |||||  
 RESULT 38  
 ABF36020/c  
 ID ABF36020 standard; DNA; 13 BP.  
 XX  
 AC ABF36020;  
 XX  
 DT 21-FEB-2002 (first entry)  
 XX  
 DE Oligonucleotide SEQ ID NO 136017 for detecting SNP TSC0033969.  
 XX  
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200177384-A2.  
 XX  
 PD 18-OCT-2001.  
 XX  
 PF 06-APR-2001; 2001WO-IB000713.  
 XX  
 PR 07-APR-2000; 2000DE-01019173.  
 XX  
 PA (EPIG-) EPIGENOMICS AG.  
 XX  
 PI Olek A, Piepenbrock C, Berlin K;  
 XX  
 DR WPI; 2001-657177/75.  
 XX  
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 PS Claim 1; SEQ ID NO 136017; 29pp + Sequence Listing; German.  
 XX  
 CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073

CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 13 BP; 3 A; 0 C; 4 G; 6 T; 0 U; 0 Other;  
 Query Match 64.7%; Score 11; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 84;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 7 AACACTCCTAT 17  
 Db 12 AACACTCCTAT 2  
 |||||  
 |||||  
 RESULT 39  
 ABC71076/c  
 ID ABC71076 standard; DNA; 13 BP.  
 XX  
 AC ABC71076;  
 XX  
 DT 21-FEB-2002 (first entry)  
 XX  
 DE Oligonucleotide SEQ ID NO 71093 for detecting SNP TSC0018437.  
 XX  
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200177384-A2.  
 XX  
 PD 18-OCT-2001.  
 XX  
 PF 06-APR-2001; 2001WO-IB000713.  
 XX  
 PR 07-APR-2000; 2000DE-01019173.  
 XX  
 PA (EPIG-) EPIGENOMICS AG.  
 XX  
 PI Olek A, Piepenbrock C, Berlin K;  
 XX  
 DR WPI; 2001-657177/75.  
 XX  
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 PS Claim 1; SEQ ID NO 71093; 29pp + Sequence Listing; German.  
 XX  
 CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 13 BP; 3 A; 0 C; 6 G; 4 T; 0 U; 0 Other;  
 Query Match 64.7%; Score 11; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 84;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 6 CAACACTCCTA 16  
 |||||  
 |||||

Db 13 CAACACTCCTTA 3

RESULT 40

ABX03942/c

ID ABX03942 standard; DNA; 15 BP.

XX AC ABX03942;

XX DT 09-JAN-2003 (first entry)

XX DE S. cerevisiae 28S rRNA fragment.

XX KW Detection; probe; diagnosis; oral disease; parodontitis; caries; therapy;

XX KW polymorphism; virulence factor; antibiotic resistance gene; prognosis;

XX KW oral infection; detection; pathogen; coronary heart disease;

XX KW diabetic symptom; ss.

XX OS Saccharomyces cerevisiae.

XX PN DE20110013-UI.

XX PD 18-OCT-2001.

XX PF 13-MAR-2001; 2001DE-02010013.

XX PR 13-MAR-2001; 2001DE-01012348.

XX PR 13-MAR-2001; 2001DE-02010013.

XX PA (ROET/) ROETGER A.

XX DR WPI; 2001-657777/76.

XX OLigonucleotide array, useful for diagnosing oral diseases, particularly

XX PT parodontitis, carries human or microbial reference sequences.

XX PS Claim 8; Page 22; 56pp; German.

XX SQ This invention describes a novel nucleotide carrier with probes used for

CC diagnosis of oral diseases, particularly parodontitis, but also caries,

CC especially to identify genetic predisposition (as indicated by

CC polymorphisms) to disease and to identify causative microorganisms or

CC their associated virulence factors and antibiotic resistance genes, e.g.

CC for selection of therapy and for prognosis. They are also useful for

CC research into oral infections. The carriers allow simultaneous detection

CC of both host and pathogen parameters, providing quickly and simply an

CC individual's parodontitis profile, including detection of pathogens that

CC are associated with increased risk of coronary heart diseases and/or

CC aggravation of diabetic symptoms, and of opportunistic pathogens.

CC ABX03870-ABX04044 represent DNA fragments used to illustrate the method

CC of the invention

XX SQ Sequence 15 BP; 5 A; 2 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 63.5%; Score 10.8; DB 1; Length 15;

Best Local Similarity 85.7%; Pred. No. 1.1e+02;

Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 AGCAGACTCCTAT 17

DB 15 AGCTACATTCCTAT 2

RESULT 41

ABH90683/c

ID ABH90683 standard; DNA; 12 BP.

XX AC ABH90683;

XX DT 22-FEB-2002 (first entry)

XX DE OLigonucleotide primer SEQ ID NO 290676 for detecting SNP TSC0014465.

XX

KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

OS Homo sapiens.

XX WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX DR WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is

XX PT designed to detect single-nucleotide polymorphisms and cytosine

XX PT methylation status.

XX SQ Claim 1; SEQ ID NO 290676; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic

CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

CC and cytosine methylation status in chemically pretreated genomic DNA. The

CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a

CC range of diseases including immune system, gastrointestinal, respiratory,

CC central nervous system, cardiovascular and metabolic disorders. The

CC oligomers are also used for detecting cell type differentiation. ABC00010

CC -ABH99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT82073

CC represent the oligomers described in the invention. NOTE: The sequence

CC data for this patent did not form part of the printed specification, but

CC was obtained in electronic format from WIPO at

CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 12 BP; 3 A; 0 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 61.2%; Score 10.4; DB 1; Length 12;

Best Local Similarity 91.7%; Pred. No. 93;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CAACACTCCTAT 17

DB 12 CAACACTCCTAT 1

RESULT 42

ABI59938/c

ID ABI59938 standard; DNA; 12 BP.

XX AC ABI59938;

XX DT 22-FEB-2002 (first entry)

XX DE OLigonucleotide primer SEQ ID NO 359911 for detecting SNP TSC0051838.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

```

XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 359911; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 4 A; 0 C; 4 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 61.2%; Score 10.4; DB 1; Length 12;
XX Best Local Similarity 91.7%; Pred. No. 93;
XX Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 6 CAACACTCCTAT 17
XX DB 12 CAACATTCCTAT 1
XX
XX RESULT 43
XX ABC51750/c
XX ID ABC51750 standard; DNA; 13 BP.
XX AC ABC51750;
XX
XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 51767 for detecting SNP TSC0014432.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB0000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 51767; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 4 A; 0 C; 4 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 61.2%; Score 10.4; DB 1; Length 13;
XX Best Local Similarity 91.7%; Pred. No. 1e+02;
XX Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 6 CAACACTCCTAT 17
XX DB 13 CAACATTCCTAT 2
XX
XX RESULT 44
XX ABF59814/c
XX ID ABF59814 standard; DNA; 13 BP.
XX AC ABF59814;
XX
XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 159811 for detecting SNP TSC0040225.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB0000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 159811; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX

```

```

SQ Sequence 13 BP; 1 A; 0 C; 6 G; 5 T; 0 U; 1 Other;
Query Match 61.2%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 1e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CAGCAACTCC 14
Db 12 CAACAACCTCC 1

RESULT 45
ABF91047
XX ABF91047 standard; DNA; 13 BP.
AC ABF91047;
XX
XX
XX 22-FEB-2002 (first entry)
DT
DE Oligonucleotide SEQ ID NO 191044 for detecting SNP TSC0047001.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
OS
XX WO200177384-A2.
PN
XX
XX 18-OCT-2001.
PD
XX
XX 06-APR-2001; 2001WO-IB000713.
PF
XX 07-APR-2000; 2000DE-01019173.
PR
XX (EPIG-) EPIGENOMICS AG.
PA
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
DR
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 191044; 29pp + Sequence Listing; German.
PS
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 3 A; 0 C; 6 G; 4 T; 0 U; 0 Other;
SQ
Query Match 61.2%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 1e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CAACAACCTCCAT 17
Db 2 CACCACCTCCAT 13

RESULT 46
ABH23826/C
XX
XX
XX ABH23826;
AC
XX
XX 22-FEB-2002 (first entry)
DT
DE Oligonucleotide SEQ ID NO 163329 for detecting SNP TSC0041059.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
OS

```





CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 13 BP; 5 A; 6 C; 0 G; 2 T; 0 U; 0 Other;  
 Query Match 61.2%; Score 10.4; DB 1; Length 13;  
 Best Local Similarity 91.7%; Pred. No. 1e+02; Mismatches 0; Gaps 0;  
 Matches 11; Conservative 0; Indels 1; Indels 0; Gaps 0;  
 QY 4 AGCAACACTCCT 15  
 DB 2 ACCAACACTCCT 13  
 RESULT 50  
 ABH62283  
 ID ABH62283 standard; DNA; 13 BP.  
 AC ABH62283;  
 XX  
 DT 22-FEB-2002 (first entry)  
 DE Oligonucleotide SEQ ID NO 262260 for detecting SNP TSC0010773.  
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200177384-A2.  
 XX  
 PD 18-OCT-2001.  
 XX  
 PF 06-APR-2001; 2001WO-IB000713.  
 XX  
 PR 07-APR-2000; 2000DE-01019173.  
 XX  
 PA (BPIG-) EPIGENOMICS AG.  
 XX  
 PI Olek A, Piepenbrock C, Berlin K;  
 XX  
 DR WPI; 2001-657177/75.  
 XX  
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 PS Claim 1; SEQ ID NO 262260; 29pp + Sequence Listing; German.  
 XX  
 CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 13 BP; 3 A; 6 C; 0 G; 4 T; 0 U; 0 Other;  
 Query Match 61.2%; Score 10.4; DB 1; Length 13;  
 Best Local Similarity 91.7%; Pred. No. 1e+02; Mismatches 1; Indels 0; Gaps 0;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CAACACTCCTAT 17  
 |||||  
 Db 1 CAACCTCCTAT 12

Search completed: November 21, 2006, 14:29:06  
 Job time : 0.001 secs

GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: November 21, 2006, 14:33:58 ; Search time 0.001 Seconds  
(without alignments)  
6.358 Million cell updates/sec

Title: US-10-823-197-7  
Perfect score: 17  
Sequence: 1 CTCAGCAACTCCTAT 17

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 0.5

Searched: 16 seqs, 187 residues

Total number of hits satisfying chosen parameters: 32

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 16 summaries

Database : rnbpndb.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	100.0	17	1	US-11-203-682-90
2	17	100.0	17	1	US-11-283-168-1
3	8.4	49.4	11	1	US-11-364-118-4
4	8.4	49.4	11	1	US-11-364-118-229
C 5	8.4	49.4	11	1	US-11-158-209-97
C 6	8.4	49.4	11	1	US-11-158-209-545
C 7	8.4	49.4	12	1	US-11-212-812A-395
C 8	8.4	49.4	12	1	US-11-212-386A-395
C 9	8	47.1	11	1	US-11-364-118-390
C 10	8	47.1	11	1	US-11-364-118-457
C 11	7.8	45.9	11	1	US-11-158-209-691
C 12	7.8	45.9	11	1	US-11-158-209-1221
C 13	7.8	45.9	11	1	US-11-148-303-66
C 14	7.4	43.5	10	1	US-10-691-012-35
C 15	7.4	43.5	10	1	US-11-148-303-23
C 16	7.4	43.5	10	1	US-11-148-303-128

ALIGNMENTS

RESULT 1  
US-11-203-682-90  
; Sequence 90, Application US/11203682  
; Publication No. US20060183161A1  
; GENERAL INFORMATION:  
; APPLICANT: Nicklin, Martin  
; APPLICANT: Barton, Jenny  
; TITLE OF INVENTION: IL-11 GENE AND POLYPEPTIDE PRODUCTS  
; FILE REFERENCE: 24299-517 CIP  
; CURRENT APPLICATION NUMBER: US/11/203,682  
; CURRENT FILING DATE: 2005-08-12  
; PRIOR APPLICATION NUMBER: 09/617,720

; PRIOR FILING DATE: 2000-07-17  
; NUMBER OF SEQ ID NOS: 132  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 90  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Chemically synthesized primer  
US-11-203-682-90

Query Match 100.0%; Score 17; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 0.25;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCAGCAACTCCTAT 17  
| | | | | | | | | | | | | | | | | |  
Db 1 CTCAGCAACTCCTAT 17

RESULT 2

US-11-283-168-1  
; Sequence 1, Application US/11283168  
; Publication No. US20060252055A1  
; GENERAL INFORMATION:  
; APPLICANT: Francis, Sheila E  
; APPLICANT: Crossman, David C  
; APPLICANT: Duff, Gordon W  
; APPLICANT: Kornman, Kenneth S  
; APPLICANT: Martinez, Katherine  
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR CARDIOVASCULAR DISORDERS  
; FILE REFERENCE: 24299-504 CIP2 CON CIP1  
; CURRENT APPLICATION NUMBER: US/11/283,168  
; CURRENT FILING DATE: 2005-11-17  
; PRIOR APPLICATION NUMBER: 10/320,360  
; PRIOR FILING DATE: 2002-12-13  
; PRIOR APPLICATION NUMBER: 09/431,352  
; PRIOR FILING DATE: 1999-11-01  
; PRIOR APPLICATION NUMBER: 09/320,395  
; PRIOR FILING DATE: 1999-05-26  
; PRIOR APPLICATION NUMBER: 08/813,456  
; PRIOR FILING DATE: 1997-03-10  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Primer  
US-11-283-168-1

Query Match 100.0%; Score 17; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 0.25;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCAGCAACTCCTAT 17  
| | | | | | | | | | | | | | | | | |  
Db 1 CTCAGCAACTCCTAT 17

RESULT 3

US-11-364-118-4  
; Sequence 4, Application US/11364118  
; Publication No. US20060204992A1  
; GENERAL INFORMATION:  
; APPLICANT: Olaf Holtkotter  
; APPLICANT: Dirk Petersohn  
; APPLICANT: Kordula Schlotmann  
; APPLICANT: Melanie Giesen  
; APPLICANT: Daniela Kessler-Becker  
; TITLE OF INVENTION: Method for Determining Hair Cycle Markers  
; FILE REFERENCE: H 06059 PCT

```
; CURRENT APPLICATION NUMBER: US/11/364.118
; CURRENT FILING DATE: 2006-02-28
; PRIOR APPLICATION NUMBER: PCT/EP2004/009435
; PRIOR FILING DATE: 2004-08-24
; PRIOR APPLICATION NUMBER: 103 40 373.6-41
; PRIOR FILING DATE: 2003-08-30
; NUMBER OF SEQ ID NOS: 570
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 4
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-364-118-4

Query Match          49.4%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 6.6;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 CAACACTCCT 15
Db      1 CAACATTCT 10
      |||||
      |||||

RESULT 4
US-11-364-118-229
; Sequence 229, Application US/11364118
; Publication No. US20060204992A1
; GENERAL INFORMATION:
; APPLICANT: Olaf Holtkotter
; APPLICANT: Dirk Petersohn
; APPLICANT: Kordula Schlottmann
; APPLICANT: Melanie Giesen
; APPLICANT: Daniela Kessler-Becker
; TITLE OF INVENTION: Method for Determining Hair Cycle Markers
; FILE REFERENCE: H 06059 PCT
; CURRENT APPLICATION NUMBER: US/11/364.118
; CURRENT FILING DATE: 2006-02-28
; PRIOR APPLICATION NUMBER: PCT/EP2004/009435
; PRIOR FILING DATE: 2004-08-24
; PRIOR APPLICATION NUMBER: 103 40 373.6-41
; PRIOR FILING DATE: 2003-08-30
; NUMBER OF SEQ ID NOS: 570
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 229
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-364-118-229

Query Match          49.4%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 6.6;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 CAACACTCCT 15
Db      1 CAACATTCT 10
      |||||
      |||||

RESULT 5
US-11-158-209-97/c
; Sequence 97, Application US/11158209
; Publication No. US2006008852A1
; GENERAL INFORMATION:
; APPLICANT: Dirk Petersohn
; APPLICANT: Kordula Schlottmann
; APPLICANT: Thomas Gassenmeier
; APPLICANT: Olaf Holtkotter
; APPLICANT: Marcus Conradt
; APPLICANT: Kay Hofmann
; TITLE OF INVENTION: Method for Determining the Homeostasis of Hairy Skin
; FILE REFERENCE: H 05667 PCT
; CURRENT APPLICATION NUMBER: US/11/158.209
; CURRENT FILING DATE: 2005-06-20
```

```
; PRIOR APPLICATION NUMBER: PCT/EP2003/014070
; PRIOR FILING DATE: 2003-12-11
; PRIOR APPLICATION NUMBER: 102 60 931.4-41
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 1335
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 97
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-158-209-97

Query Match          49.4%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 6.6;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CTCAGCAACA 10
Db      11 CCAGCAACA 2
      |||||
      |||||

RESULT 6
US-11-158-209-545/c
; Sequence 545, Application US/11158209
; Publication No. US2006008852A1
; GENERAL INFORMATION:
; APPLICANT: Dirk Petersohn
; APPLICANT: Kordula Schlottmann
; APPLICANT: Thomas Gassenmeier
; APPLICANT: Olaf Holtkotter
; APPLICANT: Marcus Conradt
; APPLICANT: Kay Hofmann
; TITLE OF INVENTION: Method for Determining the Homeostasis of Hairy Skin
; FILE REFERENCE: H 05667 PCT
; CURRENT APPLICATION NUMBER: US/11/158.209
; CURRENT FILING DATE: 2005-06-20
; PRIOR APPLICATION NUMBER: PCT/EP2003/014070
; PRIOR FILING DATE: 2003-12-11
; PRIOR APPLICATION NUMBER: 102 60 931.4-41
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 1335
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 545
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-158-209-545

Query Match          49.4%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 6.6;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 CAGCAACACT 12
Db      10 CAGCAAACT 1
      |||||
      |||||

RESULT 7
US-11-212-812A-395
; Sequence 395, Application US/11212812A
; Publication No. US20060121452A1
; GENERAL INFORMATION:
; APPLICANT: Dhallan, Ravinder S.
; TITLE OF INVENTION: METHODS FOR DETECTION OF GENETIC
; FILE REFERENCE: DISORDERS
; FILE REFERENCE: 543312000401
; CURRENT APPLICATION NUMBER: US/11/212.812A
; CURRENT FILING DATE: 2005-08-26
; PRIOR APPLICATION NUMBER: PCT/US04/006337
; PRIOR FILING DATE: 2004-03-01
; PRIOR APPLICATION NUMBER: PCT/US03/06198
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US60/378,354
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; PRIOR FILING DATE: 2002-05-08
; NUMBER OF SEQ ID NOS: 725
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 395
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-11-212-812A-395
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Query Match 49.4%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 6.1;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy 2 TCAGCAACAC 11
Db 1 TCAGTAACAC 10
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RESULT 8
US-11-212-386A-395
; Sequence 395, Application US/11212386A
; Publication No. US20060160105A1
; GENERAL INFORMATION:
; APPLICANT: Dhallan, Ravinder S.
; TITLE OF INVENTION: METHODS FOR DETECTION OF GENETIC
; FILE REFERENCE: 543312000402
; CURRENT APPLICATION NUMBER: US/11/212,386A
; CURRENT FILING DATE: 2005-08-26
; PRIOR APPLICATION NUMBER: US10/661,165
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: PCT/US03/27308
; PRIOR FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: PCT/US03/06198
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US60/378,354
; PRIOR FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 725
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 395
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-11-212-386A-395
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Best Local Similarity 90.0%; Pred. No. 6.1;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 1 TCAGTAACAC 10
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RESULT 9
US-11-364-118-390/c
; Sequence 390, Application US/11364118
; Publication No. US20060204992A1
; GENERAL INFORMATION:
; APPLICANT: Olaf Holtkötter
; APPLICANT: Dirk Petersohn
; APPLICANT: Kordula Schlotmann
; APPLICANT: Daniela Kessler-Becker
; TITLE OF INVENTION: Method for Determining Hair Cycle Markers
; FILE REFERENCE: H 06059 PCT
; CURRENT APPLICATION NUMBER: US/11/364,118
; CURRENT FILING DATE: 2006-02-28
; PRIOR APPLICATION NUMBER: PCT/EP2004/009435
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; PRIOR FILING DATE: 2004-08-24
; PRIOR APPLICATION NUMBER: 103 40 373.6-41
; PRIOR FILING DATE: 2003-08-30
; NUMBER OF SEQ ID NOS: 570
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 390
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-364-118-390
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Query Match 47.1%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 8 ACACCTCCT 15
Db 9 ACACCTCCT 2
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RESULT 10
US-11-364-118-457/c
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; Publication No. US20060204992A1
; GENERAL INFORMATION:
; APPLICANT: Olaf Holtkötter
; APPLICANT: Dirk Petersohn
; APPLICANT: Kordula Schlotmann
; APPLICANT: Melanie Giesen
; TITLE OF INVENTION: Method for Determining Hair Cycle Markers
; FILE REFERENCE: H 06059 PCT
; CURRENT APPLICATION NUMBER: US/11/364,118
; CURRENT FILING DATE: 2006-02-28
; PRIOR APPLICATION NUMBER: PCT/EP2004/009435
; PRIOR FILING DATE: 2004-08-24
; PRIOR APPLICATION NUMBER: 103 40 373.6-41
; PRIOR FILING DATE: 2003-08-30
; NUMBER OF SEQ ID NOS: 570
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 457
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-364-118-457
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Query Match 47.1%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 8 ACACCTCCT 15
Db 9 ACACCTCCT 2
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RESULT 11
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; Publication No. US2006008852A1
; GENERAL INFORMATION:
; APPLICANT: Dirk Petersohn
; APPLICANT: Kordula Schlotmann
; APPLICANT: Thomas Gassenmeier
; APPLICANT: Olaf Holtkötter
; APPLICANT: Marcus Conradt
; APPLICANT: Kay Hofmann
; TITLE OF INVENTION: Method for Determining the Homeostasis of Hairy Skin
; FILE REFERENCE: H 05667 PCT
; CURRENT APPLICATION NUMBER: US/11/158,209
; CURRENT FILING DATE: 2005-06-20
; PRIOR APPLICATION NUMBER: PCT/EP2003/014070
; PRIOR FILING DATE: 2003-12-11
; PRIOR APPLICATION NUMBER: 102 60 931.4-41
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; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 1335
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 691
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-158-209-691

Query Match      45.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 7.9;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      4 AGCAACTCTCC 14
Db      11 AGCTGCACTCC 1

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; Sequence 1221, Application US/11158209
; Publication No. US2006008852A1
; GENERAL INFORMATION:
; APPLICANT: Dirk Petersohn
; APPLICANT: Kordula Schlotmann
; APPLICANT: Thomas Gassenmeier
; APPLICANT: Olaf Holtkotter
; APPLICANT: Marcus Conrad
; APPLICANT: Kay Hofmann
; TITLE OF INVENTION: Method for Determining the Homeostasis of Hairy Skin
; FILE REFERENCE: H 05667 PCT
; CURRENT APPLICATION NUMBER: US/11/158,209
; CURRENT FILING DATE: 2005-06-20
; PRIOR APPLICATION NUMBER: PCT/EP2003/014070
; PRIOR FILING DATE: 2003-12-11
; PRIOR APPLICATION NUMBER: 102 60 931.4-41
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 1335
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 1221
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-158-209-1221

Query Match      45.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 7.9;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 CTCAGCAACAC 11
Db      11 CTCAACTACAC 1

RESULT 13
US-11-148-303-66
; Sequence 66, Application US/11148303
; Publication No. US20060154886A1
; GENERAL INFORMATION:
; APPLICANT: Gruenthal GmbH
; TITLE OF INVENTION: Regulatory elements in the 5' region of the VR1 gene
; FILE REFERENCE: GR01P003WO
; CURRENT APPLICATION NUMBER: US/11/148,303
; CURRENT FILING DATE: 2005-06-09
; NUMBER OF SEQ ID NOS: 781
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: V$NFY Q6
US-11-148-303-66

Query Match      45.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 7.9;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 CTCAGCAACAC 11
Db      11 CTCAACTACAC 1

RESULT 14
US-10-691-012-35/c
; Sequence 35, Application US/10691012
; Publication No. US20060160731A1
; GENERAL INFORMATION:
; APPLICANT: Buchardt, Ole
; APPLICANT: Egholm, Michael
; APPLICANT: Nielsen, Peter Eigil
; APPLICANT: Berg, Rolf Henrik
; TITLE OF INVENTION: Peptide Nucleic Acids
; FILE REFERENCE: IS180540
; CURRENT APPLICATION NUMBER: US/10/691,012
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: US/08/108,591
; PRIOR FILING DATE: 1993-11-22
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Novel Sequence
US-10-691-012-35

Query Match      43.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 9.8;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      9 CACTCCTAT 17
Db      10 CACTACTAT 2

RESULT 15
US-11-148-303-23
; Sequence 23, Application US/11148303
; Publication No. US20060154886A1
; GENERAL INFORMATION:
; APPLICANT: Gruenthal GmbH
; TITLE OF INVENTION: Regulatory elements in the 5' region of the VR1 gene
; FILE REFERENCE: GR01P003WO
; CURRENT APPLICATION NUMBER: US/11/148,303
; CURRENT FILING DATE: 2005-06-09
; NUMBER OF SEQ ID NOS: 781
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: V$SOX5 01
US-11-148-303-23

Query Match      43.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 9.8;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      6 CAACACTCC 14
Db      2 CAACAATCC 10
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RESULT 16
US-11-148-303-128
; Sequence 128, Application US/11148303
; Publication No. US20060154886A1
; GENERAL INFORMATION:
; APPLICANT: Gruenthal GmbH
; TITLE OF INVENTION: Regulatory elements in the 5' region of the VR1 gene
; FILE REFERENCE: GR01P003WO
; CURRENT APPLICATION NUMBER: US/11/148,303
; CURRENT FILING DATE: 2005-06-09
; NUMBER OF SEQ ID NOS: 781
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 128
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: VS0X5 01
US-11-148-303-128

Query Match      43.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 9.8;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OM nucleic - nucleic search, using sw model

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Searched: 262 seqs, 3460 residues

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Maximum Match 100%  
Listing first 262 summaries

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Pred. No. is the number of results predicted by chance to have a  
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C 114	9.4	55.3	12	1	US-10-257-017B-369661	Sequence 369661,	187	9.4	55.3	13	1	US-10-257-017B-200110	Sequence 200110,
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C 117	9.4	55.3	12	1	US-10-257-017B-379316	Sequence 379316,	C 190	9.4	55.3	13	1	US-10-257-017B-211433	Sequence 211433,
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C 119	9.4	55.3	13	1	US-10-257-017B-310	Sequence 310, App	C 192	9.4	55.3	13	1	US-10-257-017B-226549	Sequence 226549,
C 120	9.4	55.3	13	1	US-10-257-017B-24595	Sequence 24595, A	193	9.4	55.3	13	1	US-10-257-017B-226550	Sequence 226550,
C 121	9.4	55.3	13	1	US-10-257-017B-24596	Sequence 24596, A	C 194	9.4	55.3	13	1	US-10-257-017B-227085	Sequence 227085,
C 122	9.4	55.3	13	1	US-10-257-017B-25817	Sequence 25817, A	195	9.4	55.3	13	1	US-10-257-017B-227086	Sequence 227086,
C 123	9.4	55.3	13	1	US-10-257-017B-25818	Sequence 25818, A	C 196	9.4	55.3	13	1	US-10-257-017B-227087	Sequence 227087,
C 124	9.4	55.3	13	1	US-10-257-017B-25818	Sequence 25818, A	197	9.4	55.3	13	1	US-10-257-017B-227088	Sequence 227088,
C 125	9.4	55.3	13	1	US-10-257-017B-39645	Sequence 39645, A	C 198	9.4	55.3	13	1	US-10-257-017B-227088	Sequence 227088,
C 126	9.4	55.3	13	1	US-10-257-017B-39646	Sequence 39646, A	199	9.4	55.3	13	1	US-10-257-017B-231119	Sequence 231119,
C 127	9.4	55.3	13	1	US-10-257-017B-42741	Sequence 42741, A	C 200	9.4	55.3	13	1	US-10-257-017B-231120	Sequence 231120,
C 128	9.4	55.3	13	1	US-10-257-017B-42742	Sequence 42742, A	201	9.4	55.3	13	1	US-10-257-017B-233225	Sequence 233225,
C 129	9.4	55.3	13	1	US-10-257-017B-47389	Sequence 47389, A	C 202	9.4	55.3	13	1	US-10-257-017B-233226	Sequence 233226,
C 130	9.4	55.3	13	1	US-10-257-017B-47390	Sequence 47390, A	203	9.4	55.3	13	1	US-10-257-017B-235003	Sequence 235003,
C 131	9.4	55.3	13	1	US-10-257-017B-50897	Sequence 50897, A	C 204	9.4	55.3	13	1	US-10-257-017B-235004	Sequence 235004,
C 132	9.4	55.3	13	1	US-10-257-017B-50898	Sequence 50898, A	205	9.4	55.3	13	1	US-10-257-017B-248677	Sequence 248677,
C 133	9.4	55.3	13	1	US-10-257-017B-62449	Sequence 62449, A	C 206	9.4	55.3	13	1	US-10-257-017B-248678	Sequence 248678,
C 134	9.4	55.3	13	1	US-10-257-017B-62450	Sequence 62450, A	207	9.4	55.3	13	1	US-10-257-017B-259087	Sequence 259087,
C 135	9.4	55.3	13	1	US-10-257-017B-71091	Sequence 71091, A	C 208	9.4	55.3	13	1	US-10-257-017B-259088	Sequence 259088,
C 136	9.4	55.3	13	1	US-10-257-017B-71092	Sequence 71092, A	209	9.4	55.3	13	1	US-10-257-017B-263309	Sequence 263309,
C 137	9.4	55.3	13	1	US-10-257-017B-71097	Sequence 71097, A	C 210	9.4	55.3	13	1	US-10-257-017B-263310	Sequence 263310,
C 138	9.4	55.3	13	1	US-10-257-017B-71098	Sequence 71098, A	211	9.4	55.3	13	1	US-09-249-155-146	Sequence 146, App
C 139	9.4	55.3	13	1	US-10-257-017B-71101	Sequence 71101, A	C 212	9.4	55.3	13	1	US-10-314-322-146	Sequence 146, App
C 140	9.4	55.3	13	1	US-10-257-017B-71102	Sequence 71102, A	213	9.4	55.3	13	1	US-10-257-017B-274536	Sequence 274536,
C 141	9.4	55.3	13	1	US-10-257-017B-75403	Sequence 75403, A	214	9.4	55.3	13	1	US-10-257-017B-289056	Sequence 289056,
C 142	9.4	55.3	13	1	US-10-257-017B-78917	Sequence 78917, A	C 215	9.4	55.3	13	1	US-10-257-017B-304514	Sequence 304514,
C 143	9.4	55.3	13	1	US-10-257-017B-78918	Sequence 78918, A	216	9.4	55.3	13	1	US-10-257-017B-308500	Sequence 308500,
C 144	9.4	55.3	13	1	US-10-257-017B-86481	Sequence 86481, A	C 217	9.4	55.3	13	1	US-10-257-017B-318085	Sequence 318085,
C 145	9.4	55.3	13	1	US-10-257-017B-86482	Sequence 86482, A	218	9.4	55.3	13	1	US-10-257-017B-318464	Sequence 318464,
C 146	9.4	55.3	13	1	US-10-257-017B-86483	Sequence 86483, A	C 219	9.4	55.3	13	1	US-10-257-017B-331427	Sequence 331427,
C 147	9.4	55.3	13	1	US-10-257-017B-86484	Sequence 86484, A	220	9.4	55.3	13	1	US-10-257-017B-336064	Sequence 336064,
C 148	9.4	55.3	13	1	US-10-257-017B-86645	Sequence 86645, A	C 221	9.4	55.3	13	1	US-10-257-017B-349259	Sequence 349259,
C 149	9.4	55.3	13	1	US-10-257-017B-96646	Sequence 96646, A	222	9.4	55.3	13	1	US-10-257-017B-351084	Sequence 351084,
C 150	9.4	55.3	13	1	US-10-257-017B-104399	Sequence 104399,	223	9.4	55.3	13	1	US-10-257-017B-352964	Sequence 352964,
C 151	9.4	55.3	13	1	US-10-257-017B-104400	Sequence 104400,	224	8.8	51.8	12	1	US-10-257-017B-270123	Sequence 270123,
C 152	9.4	55.3	13	1	US-10-257-017B-108233	Sequence 108233,	225	8.8	51.8	12	1	US-10-257-017B-271795	Sequence 271795,
C 153	9.4	55.3	13	1	US-10-257-017B-108234	Sequence 108234,	226	8.8	51.8	12	1	US-10-257-017B-277739	Sequence 277739,
C 154	9.4	55.3	13	1	US-10-257-017B-111807	Sequence 111807,	C 227	8.8	51.8	12	1	US-10-257-017B-282732	Sequence 282732,
C 155	9.4	55.3	13	1	US-10-257-017B-111808	Sequence 111808,	228	8.8	51.8	12	1	US-10-257-017B-289048	Sequence 289048,
C 156	9.4	55.3	13	1	US-10-257-017B-117651	Sequence 117651,	229	8.8	51.8	12	1	US-10-257-017B-290054	Sequence 290054,
C 157	9.4	55.3	13	1	US-10-257-017B-117652	Sequence 117652,	230	8.8	51.8	12	1	US-10-257-017B-290876	Sequence 290876,
C 158	9.4	55.3	13	1	US-10-257-017B-127381	Sequence 127381,	231	8.8	51.8	12	1	US-10-257-017B-295767	Sequence 295767,
C 159	9.4	55.3	13	1	US-10-257-017B-127382	Sequence 127382,	232	8.8	51.8	12	1	US-10-257-017B-295767	Sequence 295767,
C 160	9.4	55.3	13	1	US-10-257-017B-127385	Sequence 127385,	C 233	8.8	51.8	12	1	US-10-257-017B-298432	Sequence 298432,
C 161	9.4	55.3	13	1	US-10-257-017B-127386	Sequence 127386,	234	8.8	51.8	12	1	US-10-257-017B-303022	Sequence 303022,
C 162	9.4	55.3	13	1	US-10-257-017B-132701	Sequence 132701,	C 235	8.8	51.8	12	1	US-10-257-017B-307432	Sequence 307432,
C 163	9.4	55.3	13	1	US-10-257-017B-132702	Sequence 132702,	236	8.8	51.8	12	1	US-10-257-017B-307496	Sequence 307496,
C 164	9.4	55.3	13	1	US-10-257-017B-136015	Sequence 136015,	C 237	8.8	51.8	12	1	US-10-257-017B-313414	Sequence 313414,
C 165	9.4	55.3	13	1	US-10-257-017B-136016	Sequence 136016,	238	8.8	51.8	12	1	US-10-257-017B-314086	Sequence 314086,
C 166	9.4	55.3	13	1	US-10-257-017B-153289	Sequence 153289,	239	8.8	51.8	12	1	US-10-257-017B-314087	Sequence 314087,
C 167	9.4	55.3	13	1	US-10-257-017B-153290	Sequence 153290,	240	8.8	51.8	12	1	US-10-257-017B-321092	Sequence 321092,
C 168	9.4	55.3	13	1	US-10-257-017B-153995	Sequence 153995,	241	8.8	51.8	12	1	US-10-257-017B-322014	Sequence 322014,
C 169	9.4	55.3	13	1	US-10-257-017B-153996	Sequence 153996,	242	8.8	51.8	12	1	US-10-257-017B-322790	Sequence 322790,
C 170	9.4	55.3	13	1	US-10-257-017B-157065	Sequence 157065,	C 243	8.8	51.8	12	1	US-10-257-017B-326438	Sequence 326438,
C 171	9.4	55.3	13	1	US-10-257-017B-157066	Sequence 157066,	244	8.8	51.8	12	1	US-10-257-017B-328173	Sequence 328173,
C 172	9.4	55.3	13	1	US-10-257-017B-169365	Sequence 169365,	C 245	8.8	51.8	12	1	US-10-257-017B-329594	Sequence 329594,
C 173	9.4	55.3	13	1	US-10-257-017B-169366	Sequence 169366,	246	8.8	51.8	12	1	US-10-257-017B-332773	Sequence 332773,
C 174	9.4	55.3	13	1	US-10-257-017B-173017	Sequence 173017,	247	8.8	51.8	12	1	US-10-257-017B-343778	Sequence 343778,
C 175	9.4	55.3	13	1	US-10-257-017B-173018	Sequence 173018,	248	8.8	51.8	12	1	US-10-257-017B-351291	Sequence 351291,
C 176	9.4	55.3	13	1	US-10-257-017B-174909	Sequence 174909,	249	8.8	51.8	12	1	US-10-257-017B-352679	Sequence 352679,
C 177	9.4	55.3	13	1	US-10-257-017B-174910	Sequence 174910,	250	8.8	51.8	12	1	US-10-257-017B-352697	Sequence 352697,
C 178	9.4	55.3	13	1	US-10-257-017B-175703	Sequence 175703,	C 251	8.8	51.8	12	1	US-10-257-017B-353232	Sequence 353232,
C 179	9.4	55.3	13	1	US-10-257-017B-175704	Sequence 175704,	252	8.8	51.8	12	1	US-10-257-017B-357288	Sequence 357288,

c 253 8.8 51.8 12 1 US-10-257-017B-360500 Sequence 360500,  
c 254 8.8 51.8 12 1 US-10-257-017B-362463 Sequence 362463,  
c 255 8.8 51.8 12 1 US-10-257-017B-367935 Sequence 367935,  
c 256 8.8 51.8 12 1 US-10-257-017B-369135 Sequence 369135,  
c 257 8.8 51.8 12 1 US-10-257-017B-370100 Sequence 370100,  
c 258 8.8 51.8 12 1 US-10-257-017B-371753 Sequence 371753,  
c 259 8.8 51.8 12 1 US-10-257-017B-374492 Sequence 374492,  
c 260 8.8 51.8 12 1 US-10-257-017B-375813 Sequence 375813,  
c 261 8.8 51.8 12 1 US-10-257-017B-379818 Sequence 379818,  
c 262 8.8 51.8 12 1 US-10-257-017B-379853 Sequence 379853,

## ALIGNMENTS

RESULT 1  
US-09-845-129-22  
; Sequence 22, Application US/09845129  
; Patent No. US20020146700A1  
; GENERAL INFORMATION:  
; APPLICANT: DUFF, GORDON W.  
; APPLICANT: COX, ANGELA  
; APPLICANT: CAMP, NICOLA J.  
; TITLE OF INVENTION: DIGTOVINE, FRANCESCO S.  
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR DISEASES ASSOCIATED  
; TITLE OF INVENTION: WITH AN IL-1 INFLAMMATORY HAPLOTYPE  
; FILE REFERENCE: MSA-010.02  
; CURRENT APPLICATION NUMBER: US/09/845,129  
; CURRENT FILING DATE: 2001-04-27  
; PRIOR APPLICATION NUMBER: 09/345,217  
; PRIOR FILING DATE: 1999-06-30  
; PRIOR APPLICATION NUMBER: PCT/GB98/01481  
; PRIOR FILING DATE: 1998-05-21  
; PRIOR APPLICATION NUMBER: 9711040.7  
; PRIOR FILING DATE: 1997-05-29  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 22  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer  
US-09-845-129-22

Query Match 100.0%; Score 17; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCAGCAACTCCTAT 17  
|||  
DB 1 CTCAGCAACTCCTAT 17

RESULT 2  
US-09-888-056A-3  
; Sequence 3, Application US/09888056A  
; Publication No. US20030124524A1  
; GENERAL INFORMATION:  
; APPLICANT: KORNMAN, KENNETH S.  
; APPLICANT: DUFF, GORDON W.  
; TITLE OF INVENTION: SCREENING ASSAYS FOR IDENTIFYING MODULATORS OF THE  
; TITLE OF INVENTION: INFLAMMATORY OR IMMUNE RESPONSE  
; FILE REFERENCE: MSA-023.01  
; CURRENT APPLICATION NUMBER: US/09/888,056A  
; CURRENT FILING DATE: 2002-05-06  
; PRIOR APPLICATION NUMBER: 60/213,853  
; PRIOR FILING DATE: 2000-06-23  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 17  
; TYPE: DNA

; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Primer  
US-09-888-056A-3

Query Match 100.0%; Score 17; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCAGCAACTCCTAT 17  
|||  
DB 1 CTCAGCAACTCCTAT 17

RESULT 3  
US-10-167-127-23  
; Sequence 23, Application US/10167127  
; Publication No. US20030100031A1  
; GENERAL INFORMATION:  
; APPLICANT: DOWER, STEVEN  
; APPLICANT: DUFF, GORDON W.  
; TITLE OF INVENTION: INTEGRATIVE ASSAYS FOR MONITORING MOLECULAR ASSEMBLY  
; TITLE OF INVENTION: EVENTS  
; FILE REFERENCE: MSA-026.01 (20974-3601)  
; CURRENT APPLICATION NUMBER: US/10/167,127  
; CURRENT FILING DATE: 2002-06-11  
; PRIOR APPLICATION NUMBER: 60/297,305  
; PRIOR FILING DATE: 2001-06-11  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 23  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Primer  
US-10-167-127-23

Query Match 100.0%; Score 17; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCAGCAACTCCTAT 17  
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DB 1 CTCAGCAACTCCTAT 17

RESULT 4  
US-10-172-919-7  
; Sequence 7, Application US/10172919  
; Publication No. US20030152947A1  
; GENERAL INFORMATION:  
; APPLICANT: CROSSMAN, DAVID C.  
; APPLICANT: DUFF, GORDON W.  
; APPLICANT: FRANCIS, SHEILA E.  
; APPLICANT: KORNMAN, KENNETH S.  
; APPLICANT: BARNETT, KATHERINE  
; TITLE OF INVENTION: METHODS FOR DETECTING AND TREATING THE EARLY ONSET OF  
; TITLE OF INVENTION: AGING-RELATED CONDITIONS  
; FILE REFERENCE: MSA-025.01  
; CURRENT APPLICATION NUMBER: US/10/172,919  
; CURRENT FILING DATE: 2002-06-17  
; PRIOR APPLICATION NUMBER: 60/298,493  
; PRIOR FILING DATE: 2001-06-15  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Primer  
US-10-172-919-7

Query Match 100.0%; Score 17; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCAGCAACACTCCTAT 17  
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Db 1 CTCAGCAACACTCCTAT 17

RESULT 5  
US-10-320-360-1  
; Sequence 1, Application US/10320360  
; Publication No. US20030175764A1  
; GENERAL INFORMATION:  
; APPLICANT: Francis, Sheila E.  
; APPLICANT: Crossman, David C.  
; APPLICANT: Duff, Gordon W.  
; APPLICANT: Kornman, Kenneth S.  
; APPLICANT: Stephenson, Katherine  
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR CARDIOVASCULAR  
; FILE REFERENCE: MSA-006.03  
; CURRENT FILING DATE: 2002-12-13  
; PRIOR APPLICATION NUMBER: US/10/320,360  
; PRIOR FILING DATE: 09/320,395  
; PRIOR FILING DATE: 1999-05-26  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer  
US-10-320-360-1

Query Match 100.0%; Score 17; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCAGCAACACTCCTAT 17  
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Db 1 CTCAGCAACACTCCTAT 17

RESULT 6  
US-10-802-061-22  
; Sequence 22, Application US/10802061  
; Publication No. US20040152124A1  
; GENERAL INFORMATION:  
; APPLICANT: DUFF, GORDON W.  
; APPLICANT: COX, ANGELA  
; APPLICANT: CAMP, NICOLA J.  
; APPLICANT: DIGIOVINE, FRANCESCO S.  
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR DISEASES ASSOCIATED  
; FILE REFERENCE: 24299-508CON3  
; CURRENT APPLICATION NUMBER: US/10/802,061  
; CURRENT FILING DATE: 2004-03-15  
; PRIOR FILING DATE: 09/845,129  
; PRIOR FILING DATE: 2001-04-27  
; PRIOR APPLICATION NUMBER: 09/345,217  
; PRIOR FILING DATE: 1999-06-30  
; PRIOR APPLICATION NUMBER: PCT/GB98/01481  
; PRIOR FILING DATE: 1998-05-21  
; PRIOR APPLICATION NUMBER: 9711040.7  
; PRIOR FILING DATE: 1997-05-29  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 22  
; LENGTH: 17  
; TYPE: DNA

; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer  
US-10-802-061-22

Query Match 100.0%; Score 17; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCAGCAACACTCCTAT 17  
| | | | | | | | | | | | | | | | | |  
Db 1 CTCAGCAACACTCCTAT 17

RESULT 7  
US-10-823-197-7  
; Sequence 7, Application US/10823197  
; Publication No. US20040229264A1  
; GENERAL INFORMATION:  
; APPLICANT: CROSSMAN, DAVID C.  
; APPLICANT: DUFF, GORDON W.  
; APPLICANT: FRANKIS, SHEILA E.  
; APPLICANT: KORNMAN, KENNETH S.  
; APPLICANT: STEPHENSON, KATHERINE  
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR RESTENOSIS  
; FILE REFERENCE: 24299-514CIP2A DIV  
; CURRENT APPLICATION NUMBER: US/10/823,197  
; CURRENT FILING DATE: 2004-04-12  
; PRIOR APPLICATION NUMBER: 09/578,534  
; PRIOR FILING DATE: 2000-05-24  
; PRIOR APPLICATION NUMBER: 09/431,352  
; PRIOR FILING DATE: 1999-11-01  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Primer  
US-10-823-197-7

Query Match 100.0%; Score 17; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCAGCAACACTCCTAT 17  
| | | | | | | | | | | | | | | | | |  
Db 1 CTCAGCAACACTCCTAT 17

RESULT 8  
US-10-712-882-5  
; Sequence 5, Application US/10712882  
; Publication No. US20050032077A1  
; GENERAL INFORMATION:  
; APPLICANT: Duff, Gordon W.  
; APPLICANT: Richardson, Robert R.S.  
; APPLICANT: Rennie, Ian G.  
; TITLE OF INVENTION: DETECTING GENETIC PREDISPOSITION TO  
; SIGHT-THREATENING DIABETIC RETINOPATHY  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP  
; STREET: One Post Office Square  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109-2170  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/712,882

FILING DATE: 12-Nov-2003

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/037,472

FILING DATE: 10-MAR-1998

APPLICATION NUMBER: PCT/GB97/02790

FILING DATE: 09-OCT-1997

ATTORNEY/AGENT INFORMATION:

NAME: Arnold, Beth E.

REGISTRATION NUMBER: 35,430

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 832-1000

TELEFAX: (617) 832-7000

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "primer"

SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-10-712-882-5

Query Match 100.0%; Score 17; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCAGCAACTCCTAT 17

Db 1 CTCAGCAACTCCTAT 17

RESULT 9

US-10-838-503-9

Sequence 9, Application US/10838503

Publication No. US2005064453A1

GENERAL INFORMATION:

APPLICANT: DUFF, GORDON

APPLICANT: KORNMAN, KENNETH

APPLICANT: VAN DIJK, SIMON

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR EARLY-ONSET MENOPAUSE

FILE REFERENCE: MSA-012.01

CURRENT APPLICATION NUMBER: US/10/838,503

CURRENT FILING DATE: 2004-05-03

NUMBER OF SEQ ID NOS: 30

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 9

LENGTH: 17

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

OTHER INFORMATION: oligonucleotide

US-10-838-503-9

Query Match 100.0%; Score 17; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCAGCAACTCCTAT 17

Db 1 CTCAGCAACTCCTAT 17

RESULT 10

US-11-121-634-22

Sequence 22, Application US/11121634

Publication No. US20050282198A1

GENERAL INFORMATION:

APPLICANT: Duff, Gordon  
TITLE OF INVENTION: Diagnostics and Therapeutics for Diseases Associated with an IL-1  
FILE REFERENCE: 24299-508CON3 CIP1  
CURRENT APPLICATION NUMBER: US/11/121,634  
CURRENT FILING DATE: 2005-05-03  
PRIOR APPLICATION NUMBER: US 10/802,061  
PRIOR FILING DATE: 2004-03-15  
PRIOR APPLICATION NUMBER: US 09/845,129  
PRIOR FILING DATE: 2001-04-27  
PRIOR APPLICATION NUMBER: US 09/345,217  
PRIOR FILING DATE: 1999-06-30  
PRIOR APPLICATION NUMBER: PCT/GB98/01481  
PRIOR FILING DATE: 1998-05-21  
PRIOR APPLICATION NUMBER: GB9711040.7  
PRIOR FILING DATE: 1997-05-29  
PRIOR APPLICATION NUMBER: US 10/300,011  
PRIOR FILING DATE: 2002-11-19  
PRIOR APPLICATION NUMBER: US 60/386,020  
PRIOR FILING DATE: 2002-06-05  
PRIOR APPLICATION NUMBER: US 60/331,681  
PRIOR FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: US 60/567,727  
PRIOR FILING DATE: 2004-05-03  
NUMBER OF SEQ ID NOS: 202  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 22  
LENGTH: 17  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: chemically synthesized primer  
US-11-121-634-22

Query Match 100.0%; Score 17; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCAGCAACTCCTAT 17

Db 1 CTCAGCAACTCCTAT 17

RESULT 11

US-10-626-830-9

Sequence 9, Application US/10626830

Publication No. US2004022928A1

GENERAL INFORMATION:

APPLICANT: Sims, John E.

APPLICANT: Kaufman, Dixon B.

TITLE OF INVENTION: IL-1 Genotype in Early Kidney Allograft Rejection

FILE REFERENCE: WESTERN-08309

CURRENT APPLICATION NUMBER: US/10/626,830

CURRENT FILING DATE: 2003-07-24

NUMBER OF SEQ ID NOS: 18

SOFTWARE: PatentIn version 3.2

SEQ ID NO 9

LENGTH: 17

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetic

US-10-626-830-9

Query Match 82.4%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 35;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCAGCAACTCC 14

Db 4 CTCAGCAACTCC 17

## RESULT 12

US-11-083-784-1215680/c  
; Sequence 1215680, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR FILING DATE: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1215680  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-1215680

Query Match 82.4%; Score 14; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CAGCAACACTCCTA 16  
| | | | | | | | | | | | | | | | | |  
Db 16 CAGCAACACTCCTA 3

## RESULT 13

US-11-083-784-1215694/c  
; Sequence 1215694, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR FILING DATE: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1215694  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-1215694

Query Match 82.4%; Score 14; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CAGCAACACTCCTA 16  
| | | | | | | | | | | | | | | | | |

## Db 15 CAGCAACACTCCTA 2

RESULT 14  
US-11-083-784-1215717/c  
; Sequence 1215717, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR FILING DATE: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1215717  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-1215717

Query Match 82.4%; Score 14; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CAGCAACACTCCTA 16  
| | | | | | | | | | | | | | | | | |  
Db 17 CAGCAACACTCCTA 4

## RESULT 15

US-11-101-244-1215680/c  
; Sequence 1215680, Application US/1101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1215680  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-1215680

Query Match 82.4%; Score 14; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CAGCAACACTCCTA 16



```
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1372880
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
;
US-11-083-784-1372880

Query Match      81.2%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 42;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CTCAGCAACACTCCTAT 17
   ||||| ||||| |||||
Db 19 CTCAACTACACTCCTAT 3
```

```
RESULT 21
US-11-101-244-921461
; Sequence 921461, Application US/11/01244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/012,444
; CURRENT FILING DATE: 2005-04-07
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 921461
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
;
US-11-101-244-921461

Query Match      81.2%; Score 13.8; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 42;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CTCAGCAACACTCCTAT 17
   ||||| ||||| |||||
Db 1 CUCAGCAUCUCUCCUAU 17

RESULT 22
US-11-101-244-1372880/c
```

```
; Sequence 1372880, Application US/11/01244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/012,444
; CURRENT FILING DATE: 2005-04-07
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1372880
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
;
US-11-101-244-1372880

Query Match      81.2%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 42;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CTCAGCAACACTCCTAT 17
   ||||| ||||| |||||
Db 19 CTCAACTACACTCCTAT 3
```

```
RESULT 23
US-11-083-784-628637/c
; Sequence 628637, Application US/11/083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 628637
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
;
US-11-083-784-628637

Query Match      78.8%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 47;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTCAGCAACACTCCT 15
   ||||| ||||| |||||
Db 18 CTCAGAAACACTCCT 4

RESULT 24
```



US-11-083-784-628845/c  
; Sequence 628845, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 134990S  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 628845  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-628845

Query Match 78.8%; Score 13.4; DB 1; Length 19;  
Best Local Similarity 93.3%; Pred. No. 47;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 1 CTCAGCAACACTCCT 15  
| | | | | | | | | | | | | | | | | |  
Db 18 CTCAGAAACACTCCT 4

RESULT 25  
US-11-101-244-628637/c  
; Sequence 628637, Application US/1101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 134990S  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 628637  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-628637

Query Match 78.8%; Score 13.4; DB 1; Length 19;  
Best Local Similarity 93.3%; Pred. No. 47;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 1 CTCAGCAACACTCCT 15  
| | | | | | | | | | | | | | | | | |  
Db 18 CTCAGAAACACTCCT 4

RESULT 26  
US-11-101-244-628845/c  
; Sequence 628845, Application US/1101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 134990S  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 628845  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-628845

Query Match 78.8%; Score 13.4; DB 1; Length 19;  
Best Local Similarity 93.3%; Pred. No. 47;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 1 CTCAGCAACACTCCT 15  
| | | | | | | | | | | | | | | | | |  
Db 18 CTCAGAAACACTCCT 4

RESULT 27  
US-10-310-914A-273305/c  
; Sequence 273305, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087,0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: Patent in version 3.3  
; SEQ ID NO 273305  
; LENGTH: 18  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-273305

Query Match 75.3%; Score 12.8; DB 1; Length 18;  
Best Local Similarity 87.5%; Pred. No. 52;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
Qy 1 CTCAGCAACACTCCTA 16  
| | | | | | | | | | | | | | | | | |  
Db 16 CCCAGCAACCTCCTA 1

RESULT 28  
US-10-096-125-14/c  
; Sequence 14, Application US/10096125  
; Publication No. US20030077608A1  
; GENERAL INFORMATION:  
; APPLICANT: Coull, James M.  
; APPLICANT: Fiandaca, Mark J.  
; APPLICANT: Kristjanson, Mark D.

; APPLICANT: Hyldeg-Nielsen, Jens J.  
; APPLICANT: Creasey, Theresa S.  
; TITLE OF INVENTION: Methods, Kits And Compositions Pertaining To  
; TITLE OF INVENTION: Combination Oligomers And Libraries For Their  
; TITLE OF INVENTION: Preparation  
; FILE REFERENCE: B20102-US  
; CURRENT APPLICATION NUMBER: US/10/096,125  
; CURRENT FILING DATE: 2002-03-09  
; PRIOR APPLICATION NUMBER: 60/274,547  
; PRIOR FILING DATE: 2001-03-09  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 16  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Oligonucleotide Primer  
US-10-096-125-14

Query Match 72.9%; Score 12.4; DB 1; Length 16;  
Best Local Similarity 92.9%; Pred. No. 51;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TCAGCAACACTCCT 15  
Db 15 TCAGCAACACTCCT 2

## RESULT 29

US-10-257-017B-302368/c  
; Sequence 302368, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 302368  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0019966

US-10-257-017B-302368  
Query Match 64.7%; Score 11; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 56;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CAACACTCCTTA 16  
Db 11 CAACACTCCTTA 1

## RESULT 30

US-10-257-017B-71093/c  
; Sequence 71093, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 136017

; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 71093  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0018437  
US-10-257-017B-71093

Query Match 64.7%; Score 11; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CAACACTCCTTA 16  
Db 13 CAACACTCCTTA 3

## RESULT 31

US-10-257-017B-71094  
; Sequence 71094, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 71094  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0018437

US-10-257-017B-71094  
Query Match 64.7%; Score 11; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CAACACTCCTTA 16  
Db 1 CAACACTCCTTA 11

## RESULT 32

US-10-257-017B-136017/c  
; Sequence 136017, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 136017

```
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0033969
US-10-257-017B-136017

Query Match      64.7%; Score 11; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 AACACTCCTAT 17
Db 12 AACACTCCTAT 2

RESULT 33
US-10-257-017B-136018
; Sequence 136018, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 136018
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0033969
US-10-257-017B-136018

Query Match      64.7%; Score 11; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 AACACTCCTAT 17
Db 2 AACACTCCTAT 12

RESULT 34
US-09-848-754A-9312
; Sequence 9312, Application US/09848754A
; Publication No. US20030073207A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; TITLE OF INVENTION: Levels of Epidermal Growth Factor Receptors
; FILE REFERENCE: MBH00-958-1 (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9312
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic acid
US-09-848-754A-9312

Query Match      63.5%; Score 10.8; DB 1; Length 15;
Best Local Similarity 71.4%; Pred. No. 75;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 2 TCAGCAACTCCT 15
Db 2 UCAGCAACAACCU 15

RESULT 35
US-10-257-017B-290676/c
; Sequence 290676, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 290676
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0014465
US-10-257-017B-290676

Query Match      61.2%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 66;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CAACACTCCTAT 17
Db 12 CAACACTCCTAT 1

RESULT 36
US-10-257-017B-359911/c
; Sequence 359911, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 359911
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0051838
US-10-257-017B-359911

Query Match      61.2%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 66;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CAACACTCCTAT 17
Db 12 CAACACTCCTAT 1

RESULT 37
```

```

US-10-257-017B-51767/c
; Sequence 51767, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 51767
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0014432
US-10-257-017B-51767

Query Match      61.2%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 72;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      6 CAACACTCCTAT 17
Db      13 CAACATTCCTAT 2

RESULT 38
US-10-257-017B-51768
; Sequence 51768, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 51768
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0014432
US-10-257-017B-51768

Query Match      61.2%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 72;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      6 CAACACTCCTAT 17
Db      1 CAACATTCCTAT 12

RESULT 39
US-10-257-017B-159811/c
; Sequence 159811, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin

```

```

; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 159811
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0040225
US-10-257-017B-159811

Query Match      61.2%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 72;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      3 CAGCAACACTCC 14
Db      12 CAACACACTCC 1

RESULT 40
US-10-257-017B-159812
; Sequence 159812, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 159812
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0040225
US-10-257-017B-159812

Query Match      61.2%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 72;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      3 CAGCAACACTCC 14
Db      2 CAACACACTCC 13

RESULT 41
US-10-257-017B-163329/c
; Sequence 163329, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07

```

US-10-257-017B-163329  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 163329  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0041059  
US-10-257-017B-163329

Query Match 61.2%; Score 10.4; DB 1; Length 13;  
Best Local Similarity 91.7%; Pred. No. 72;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 AGCAACTCTCT 15  
Db 12 ACCAACTCTCT 1

## RESULT 42

US-10-257-017B-163330  
; Sequence 163330, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 163330  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0041059  
US-10-257-017B-163330

Query Match 61.2%; Score 10.4; DB 1; Length 13;  
Best Local Similarity 91.7%; Pred. No. 72;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 AGCAACTCTCT 15  
Db 2 ACCAACTCTCT 13

## RESULT 43

US-10-257-017B-179987/c  
; Sequence 179987, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 179987  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0044568

US-10-257-017B-179987

Query Match 61.2%; Score 10.4; DB 1; Length 13;  
Best Local Similarity 91.7%; Pred. No. 72;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTCAGCAACT 12  
Db 12 CTCATCAACT 1

## RESULT 44

US-10-257-017B-179988  
; Sequence 179988, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 179988  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0044568  
US-10-257-017B-179988

Query Match 61.2%; Score 10.4; DB 1; Length 13;  
Best Local Similarity 91.7%; Pred. No. 72;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTCAGCAACT 12  
Db 2 CTCATCAACT 13

## RESULT 45

US-10-257-017B-191043/c  
; Sequence 191043, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 191043  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0047001  
US-10-257-017B-191043

Query Match 61.2%; Score 10.4; DB 1; Length 13;  
Best Local Similarity 91.7%; Pred. No. 72;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CAACACTCTAT 17

Db 12 CACCACCTCCTAT 1  
||| ||||| |||||

## RESULT 46

US-10-257-017B-191044  
; Sequence 191044, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; PRIOR FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 191044  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0047001  
US-10-257-017B-191044

Query Match 61.2%; Score 10.4; DB 1; Length 13;  
Best Local Similarity 91.7%; Pred. No. 72;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CACCACCTCCTAT 17  
||| ||||| |||||  
Db 2 CACCACCTCCTAT 13

## RESULT 47

US-10-257-017B-222887/c  
; Sequence 222887, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; PRIOR FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 222887  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0006573  
US-10-257-017B-222887

Query Match 61.2%; Score 10.4; DB 1; Length 13;  
Best Local Similarity 91.7%; Pred. No. 72;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CACCACCTCCTAT 17  
||| ||||| |||||  
Db 13 CAAAACCTCCTAT 2

## RESULT 48

US-10-257-017B-222888  
; Sequence 222888, Application US/10257017B

; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; PRIOR FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 222888  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0006573  
US-10-257-017B-222888

Query Match 61.2%; Score 10.4; DB 1; Length 13;  
Best Local Similarity 91.7%; Pred. No. 72;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CACCACCTCCTAT 17  
||| ||||| |||||  
Db 1 CAAAACCTCCTAT 12

## RESULT 49

US-10-257-017B-223803/c  
; Sequence 223803, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 223803  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0054492  
US-10-257-017B-223803

Query Match 61.2%; Score 10.4; DB 1; Length 13;  
Best Local Similarity 91.7%; Pred. No. 72;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CACCACCTCCTAT 17  
||| ||||| |||||  
Db 13 CAAAACCTCCTAT 2

## RESULT 50

US-10-257-017B-223804  
; Sequence 223804, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 223804  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0054492  
US-10-257-017B-223804

; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 223804  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0054492  
US-10-257-017B-223804

Query Match 61.2%; Score 10.4; DB 1; Length 13;  
Best Local Similarity 91.7%; Pred. No. 72;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 6 CAACACTCCTAT 17  
|||||  
Db 1 CAACATTCCTAT 12

Search completed: November 21, 2006, 14:32:49  
Job time : 0.001 secs

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OM nucleic - nucleic search, using sw model

Run on: November 21, 2006, 14:35:21 ; Search time 0.001 Seconds  
(without alignment)  
0.986 Million cell updates/sec

Title: US-10-823-197-7  
Perfect score: 17  
Sequence: 1 CTCAGCAACTCCTAT 17

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 0.5

Searched: 3 seqs, 29 residues

Total number of hits satisfying chosen parameters: 6

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 3 summaries

Database : rstdb:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8.4	49.4	12	1	CF543243
C 2	6.4	37.6	9	1	CF543243
C 3	6	35.3	8	1	CL659535

# ALIGNMENTS

RESULT 1  
LOCUS CF543243 12 bp mRNA linear EST 22-SEP-2003  
DEFINITION S014680-024-030-N02-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone 024-030-N02 5-PRIME, mRNA sequence.  
ACCESSION CF543243  
VERSION CF543243.1 GI:34891683  
KEYWORDS EST.  
SOURCE Beta vulgaris  
ORGANISM Beta vulgaris  
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Amaranthaceae; Beta.  
AUTHORS 1 (bases 1 to 12)  
Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.  
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes  
JOURNAL Plant J. 32 (5), 845-857 (2002)  
PUBMED 12472698  
COMMENT Contact: Weishaar B  
ADIS DNA core facility at MP1Z  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany

## FEATURES

source

1. .12  
/organism="Beta vulgaris"  
/mol\_type="mRNA"  
/cultivar="KWS2320 (double haploid, monogerm breeding line)"  
/db\_xref="GABI:936512"  
/db\_xref="taxon:161934"  
/clone="024-030-N02"  
/tissue\_type="leaf"  
/lab\_host="EMDH10B"  
/clone\_lib="MP1Z-ADIS-024-leaf"  
/note="Vector: pCMVSPORT6; Site1: Sali; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatgut AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:  
SP6-Sali-CCAGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database:http://gabi.rzpd.de"

Query Match 49.4%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 0;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTCAGCAACA 10  
Dd 2 CTCAGCAACA 11

## RESULT 2

DR026242/c  
LOCUS DR026242 9 bp mRNA linear EST 26-MAY-2005  
DEFINITION Osmo0110 F. cylindrus osmotic stress library Fragilariopsis  
cylindrus cDNA clone FcyleSta35b12.sl, mRNA sequence.  
ACCESSION DR026242  
VERSION DR026242.1 GI:66748605  
KEYWORDS EST.  
SOURCE Fragilariopsis cylindrus  
ORGANISM Fragilariopsis cylindrus  
REFERENCE 1 (bases 1 to 9)  
Krell,A. and Gloeckner,G.  
AUTHORS Analysis of an osmotic stress induced cDNA library of the  
TITLE psychrophilic diatom Fragilariopsis cylindrus  
JOURNAL Unpublished (2004)  
COMMENT Contact: Krell, Andreas; Gloeckner, Gernot  
Biological Oceanography, Sea ice research; Genome Analysis  
Alfred-Wegner-Institute for Polar and Marine Research; Institute  
for Molecular Biotechnology  
Am Handelshafen 12, D-27570 Bremerhaven, Germany; Beutenbergstr.  
11, D-07745 Jena, Germany  
Tel: ++49 471 48311812; ++49 3641 656440  
Fax: ++49 471 48311425; ++49 3641 656255  
Email: akrell@awi-bremerhaven.de; gernot@imb-jena.de  
PCR Primers  
FORWARD: 5'M13  
BACKWARD: 3'M13  
Seq primer: 5'GTAAACGACGGCCAG 3'.  
Location/Qualifiers  
1. .9  
/organism="Fragilariopsis cylindrus"  
/mol\_type="mRNA"  
/db\_xref="taxon:186039"  
/clone="FcyleSta35b12.sl"

## FEATURES

source  
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/organism="Fragilariopsis cylindrus"  
/mol\_type="mRNA"  
/db\_xref="taxon:186039"  
/clone="FcyleSta35b12.sl"

Fax: 00492215062851  
Email: weishaa@mplz-koeln.mpg.de  
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Seq primer: SP6.  
Location/Qualifiers  
1. .12

Search completed: November 21, 2006, 14:35:21  
Job time : 0.001 secs



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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-628-282-1

Query Match 100.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.083;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCAGCAACACTCCTAT 17
Db 1 CTCAGCAACACTCCTAT 17

RESULT 2
US-08-587-911-1
; Sequence 1, Application US/08587911
; Patent No. 5942390
; GENERAL INFORMATION:
; APPLICANT: Cominelli M.D., Fabio
; APPLICANT: Pizarro Ph.D., Theresa
; APPLICANT: Rotter M.D., Jerome I.
; APPLICANT: Yang M.D., Huiying
; TITLE OF INVENTION: METHODS OF SCREENING FOR ULCERATIVE
; TITLE OF INVENTION: COLITIS BY DETECTING AN INTERLEUKIN-1 RECEPTOR ANTAGONIST
; TITLE OF INVENTION: POLYMORPHISM
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/587,911
; FILING DATE: January 12, 1996
; CLASSIFICATION: 538
; ATTORNEY/AGENT INFORMATION:
; NAME: Whiteford Esq., Wendy A
; REGISTRATION NUMBER: 36,964
; REFERENCE/DOCKET NUMBER: P07 34246
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 213-622-7700
; TELEFAX: 213-489-4210
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
US-08-587-911-1

Query Match 100.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.083;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCAGCAACACTCCTAT 17
Db 1 CTCAGCAACACTCCTAT 17

RESULT 3
US-08-813-456-1
; Sequence 1, Application US/08813456
; Patent No. 6210877
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; GENERAL INFORMATION:
; APPLICANT: Francis, Sheila
; APPLICANT: Crossman, David
; APPLICANT: Duff, Gordon
; TITLE OF INVENTION: Prediction of Coronary Artery
; TITLE OF INVENTION: Disease
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jenkins & Gilchrist
; STREET: 1100 Louisiana, Suite 1800
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/813,456
; FILING DATE: 10-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Turley, Charles P
; REGISTRATION NUMBER: 35,723
; REFERENCE/DOCKET NUMBER: 33174-00003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713)9513310
; TELEFAX: (713)9513314
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-813-456-1

Query Match 100.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.083;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCAGCAACACTCCTAT 17
Db 1 CTCAGCAACACTCCTAT 17

RESULT 4
US-09-345-217-22
; Sequence 22, Application US/09345217
; Patent No. 6268142
; GENERAL INFORMATION:
; APPLICANT: DUFF, GORDON W.
; APPLICANT: COX, ANGELA
; APPLICANT: CAMP, NICOLA J.
; APPLICANT: DIGIOVINE, FRANCESCO S.
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR DISEASES ASSOCIATED
; TITLE OF INVENTION: WITH AN IL-1 INFLAMMATORY HAPLOTYPE
; FILE REFERENCE: MSA-010.02
; CURRENT APPLICATION NUMBER: US/09/345,217
; CURRENT FILING DATE: 1999-06-30
; EARLIER APPLICATION NUMBER: PCT/GB98/01481
; EARLIER FILING DATE: 1998-05-21
; EARLIER APPLICATION NUMBER: 9711040.7
; EARLIER FILING DATE: 1997-05-29
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
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; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-345-217-22

Query Match          100.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.083;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCAGCAACACTCCTAT 17
Db 1 CTCAGCAACACTCCTAT 17

RESULT 5
US-09-431-352-1
; Sequence 1, Application US/09431352
; Patent No. 6524795
; GENERAL INFORMATION:
; APPLICANT: Francis, Sheila E.
; APPLICANT: Crossman, David C.
; APPLICANT: Duff, Gordon W.
; APPLICANT: Kornman, Kenneth S.
; APPLICANT: Stephenson, Katherine
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR CARDIOVASCULAR
; TITLE OF INVENTION: DISORDERS
; FILE REFERENCE: MSA-006.03
; CURRENT APPLICATION NUMBER: US/09/431,352
; CURRENT FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: 09/320,395
; PRIOR FILING DATE: 1999-05-26
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-431-352-1

Query Match          100.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.083;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCAGCAACACTCCTAT 17
Db 1 CTCAGCAACACTCCTAT 17

RESULT 6
US-09-845-129-22
; Sequence 22, Application US/09845129
; Patent No. 6706478
; GENERAL INFORMATION:
; APPLICANT: DUFF, GORDON W.
; APPLICANT: COX, ANGELA
; APPLICANT: CAMP, NICOLA J.
; APPLICANT: DIGIOVINE, FRANCESCO S.
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR DISEASES ASSOCIATED
; TITLE OF INVENTION: WITH AN IL-1 INFLAMMATORY HAPLOTYPE
; FILE REFERENCE: MSA-010.02
; CURRENT APPLICATION NUMBER: US/09/845,129
; CURRENT FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: 09/345,217
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: PCT/GB98/01481
; PRIOR FILING DATE: 1998-05-21
; PRIOR APPLICATION NUMBER: 9711040.7
; PRIOR FILING DATE: 1997-05-29
; NUMBER OF SEQ ID NOS: 32

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-845-129-22

Query Match          100.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.083;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCAGCAACACTCCTAT 17
Db 1 CTCAGCAACACTCCTAT 17

RESULT 7
US-09-037-472-5
; Sequence 5, Application US/09037472
; Patent No. 6713253
; GENERAL INFORMATION:
; APPLICANT: Duff, Gordon W.
; APPLICANT: Richardson, Robert R.S.
; APPLICANT: Rennie, Ian G.
; TITLE OF INVENTION: DETECTING GENETIC PREDISPOSITION TO
; TITLE OF INVENTION: SIGHT-THREATENING DIABETIC RETINOPATHY
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/037,472
; FILING DATE: 10-MAR-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB97/02790
; FILING DATE: 09-OCT-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 832-1000
; TELEFAX: (617) 832-7000
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "primer"
US-09-037-472-5

Query Match          100.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.083;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCAGCAACACTCCTAT 17
Db 1 CTCAGCAACACTCCTAT 17
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RESULT 8
US-09-578-534-7
; Sequence 7, Application US/09578534
; Patent No. 6720141
; GENERAL INFORMATION:
; APPLICANT: CROSSMAN, DAVID C.
; APPLICANT: DUFF, GORDON W.
; APPLICANT: FRANCIS, SHEILA E.
; APPLICANT: KORNMAN, KENNETH S.
; APPLICANT: STEPHENSON, KATHERINE
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR RESTENOSIS
; FILE REFERENCE: MSA-017.02
; CURRENT APPLICATION NUMBER: US/09/578,534
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: 09/431,352
; PRIOR FILING DATE: 1999-11-01
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-578-534-7

Query Match      100.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.083;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCAGCAACACTCCTAT 17
Db 1 CTCAGCAACACTCCTAT 17

RESULT 9
US-09-632-657-9
; Sequence 9, Application US/09632657
; Patent No. 6730476
; GENERAL INFORMATION:
; APPLICANT: DUFF, GORDON
; APPLICANT: KORNMAN, KENNETH
; APPLICANT: VAN DIJK, SIMON
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR EARLY-ONSET MENOPAUSE
; FILE REFERENCE: MSA-012.01
; CURRENT APPLICATION NUMBER: US/09/632,657
; CURRENT FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-632-657-9

Query Match      100.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.083;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCAGCAACACTCCTAT 17
Db 1 CTCAGCAACACTCCTAT 17

RESULT 10
US-09-693-555A-15
; Sequence 15, Application US/09693555A
; Patent No. 6733967
; GENERAL INFORMATION:
; APPLICANT: KORNMAN, KENNETH
; APPLICANT: DUFF, GORDON
; APPLICANT: OFFENBACHER, STEVEN
; TITLE OF INVENTION: PETAL TESTING FOR PREDICTION OF LOW BIRTH WEIGHT
; FILE REFERENCE: MSA-009.01
; CURRENT APPLICATION NUMBER: US/09/693,555A
; CURRENT FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: PCT/US99/08794
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/082,487
; PRIOR FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-693-555A-15

Query Match      100.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.083;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCAGCAACACTCCTAT 17
Db 1 CTCAGCAACACTCCTAT 17

RESULT 11
US-09-584-950-13
; Sequence 13, Application US/09584950
; Patent No. 6746839
; GENERAL INFORMATION:
; APPLICANT: DUFF, GORDON W.
; APPLICANT: DI GIOVINE, FRANCESCO S.
; APPLICANT: BARNES, PETER J.
; APPLICANT: LIM, SAMSON
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR AN OBSTRUCTIVE AIRWAY
; FILE REFERENCE: MSA-005.02
; CURRENT APPLICATION NUMBER: US/09/584,950
; CURRENT FILING DATE: 2000-06-01
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-584-950-13

Query Match      100.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.083;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCAGCAACACTCCTAT 17
Db 1 CTCAGCAACACTCCTAT 17

RESULT 12
US-08-373-124A-95/c
; Sequence 95, Application US/08373124A
; Patent No. 5646042
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth
; APPLICANT: McSwiggen, James
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
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; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
; TITLE OF INVENTION: CANCER USING RIBOZYMES
; NUMBER OF SEQUENCES: 2627
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/373,124A
; FILING DATE: January 13, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; APPLICATION NUMBER: 08/192,943
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: 07/987,132
; FILING DATE: December 7, 1992
; APPLICATION NUMBER: 07/936,422
; FILING DATE: August 26, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 95:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-373-124A-95

Query Match 63.5%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 2.3;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTCAGCAACACTCC 14
Db 14 CTCAGCAACATTC 1

RESULT 13
US-08-435-628-95/c
; Sequence 95, Application US/08435628
; Patent No. 5817796
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth
; APPLICANT: McSwigen, James
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
; TITLE OF INVENTION: CANCER USING RIBOZYMES
; NUMBER OF SEQUENCES: 2627
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California

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; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,628
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/373,124
; FILING DATE: January 13, 1995
; APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; APPLICATION NUMBER: 08/192,943
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: 07/987,132
; FILING DATE: December 7, 1992
; APPLICATION NUMBER: 07/936,422
; FILING DATE: August 26, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 95:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-435-628-95

Query Match 63.5%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 2.3;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTCAGCAACACTCC 14
Db 14 CTCAGCAACATTC 1

RESULT 14
US-09-249-155A-146/c
; Sequence 146, Application US/09249155A
; Patent No. 6538173
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; TITLE OF INVENTION: Healing
; FILE REFERENCE: 00486,78503
; CURRENT APPLICATION NUMBER: US/09/249,155A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,737
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/097,937
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: US 60/102,051
; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 146
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
; US-09-249-155A-146

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Query Match      52.9%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CTCAGCAAC 9
Db      9 CTCAGCAAC 1

RESULT 15
US-09-491-356C-10
; Sequence 10 Application US/09491356C
; Patent No. 6566361
; GENERAL INFORMATION:
; APPLICANT: Philibert, Robert A.
; APPLICANT: Ginns, Edward I.
; APPLICANT: Delisi, Lynn
; TITLE OF INVENTION: IDENTIFICATION OF POLYMORPHISMS IN THE PCTG4 REGION OF XQ13
; FILE REFERENCE: 9465.6US11
; CURRENT APPLICATION NUMBER: US/09/491.356C
; CURRENT FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: PCT/US99/09365
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 60/083,465
; PRIOR FILING DATE: 1998-04-29
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-491-356C-10

Query Match      52.9%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 CAGCAACAC 11
Db      1 CAGCAACAC 9

RESULT 16
US-09-281-418-146
; Sequence 146 Application US/09281418
; Patent No. 6287769
; GENERAL INFORMATION:
; APPLICANT: Inoue, Takakazu
; TITLE OF INVENTION: Method of Amplifying DNA Fragment, Apparatus for Amplifying DNA F
; TITLE OF INVENTION: agent, Method of Assaying Microorganisms, Method of Analyzing Mi
; TITLE OF INVENTION: niems and Method of Assaying Contaminant
; FILE REFERENCE: 9982-7
; CURRENT APPLICATION NUMBER: US/09/281.418
; CURRENT FILING DATE: 1999-03-30
; EARLIER APPLICATION NUMBER: JP/1998/87651
; EARLIER FILING DATE: 1998-03-31
; EARLIER APPLICATION NUMBER: JP/1999/69694
; EARLIER FILING DATE: 1999-03-16
; NUMBER OF SEQ ID NOS: 216
; SEQ ID NO 146
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-281-418-146

Query Match      49.4%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 9.6;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 CTCAGCAACA 10
Db      1 CTCAGCAACA 10
```

```
Db      2 CTCAGCAACA 11

RESULT 17
US-09-210-952-39/c
; Sequence 39 Application US/09210952A
; Patent No. 6624288
; GENERAL INFORMATION:
; APPLICANT: Fainzilber, Michael M.
; APPLICANT: Kits, Karel S.
; APPLICANT: Burlingame, Alma L.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Walker, Craig
; APPLICANT: Watkins, Maren
; APPLICANT: Shetty, Reshma
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Imperial, Julita
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Vrije Universiteit
; APPLICANT: Regents of the University of California
; TITLE OF INVENTION: Gamma-Conopeptides
; FILE REFERENCE: Gamma-Conopeptides
; CURRENT APPLICATION NUMBER: US/09/210.952A
; CURRENT FILING DATE: 1998-12-15
; EARLIER APPLICATION NUMBER: US 60/069,706
; EARLIER FILING DATE: 1997-12-16
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:degenerate
; OTHER INFORMATION: probe for consensus gamma-conopeptide sequence.
US-09-210-952-39

Query Match      49.4%; Score 8.4; DB 1; Length 12;
Best Local Similarity 60.0%; Pred. No. 9.6;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy      4 AGCAACACTC 13
Db      10 ARCAACAYTS 1

RESULT 18
US-09-990-186-2463/c
; Sequence 2463 Application US/09990186
; Patent No. 7030215
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990.186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2463
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-2463

Query Match      47.1%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```



Qy 7 AACACTCC 14  
|||||  
Db 8 AACACTCC 1

## RESULT 19

US-09-990-186-2464/c

; Sequence 2464, Application US/09990186

; Patent No. 7030215

; GENERAL INFORMATION:

; APPLICANT: LIU, Qiang

; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE

; FILE REFERENCE: 8325-0011.21 / S11-US3

; CURRENT APPLICATION NUMBER: US/09/990,186

; CURRENT FILING DATE: 2001-11-20

; NUMBER OF SEQ ID NOS: 4085

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2464

; LENGTH: 9

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: example target

; OTHER INFORMATION: DNA

US-09-990-186-2464

## Query Match

Best Local Similarity 47.1%; Score 8; DB 1; Length 9;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 AACACTCC 14  
|||||  
Db 8 AACACTCC 1

## RESULT 20

US-09-508-753B-65

; Sequence 65, Application US/09508753B

; Patent No. 6544736

; GENERAL INFORMATION:

; APPLICANT: Akira SHIMAMOTO

; APPLICANT: Yasuhiro FURUICHI

; APPLICANT: Yuko SHIBATA

; APPLICANT: Hiroko FUNAKI

; APPLICANT: Eiiji OHARA

; APPLICANT: Masanori WATAHIKI

; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample

; FILE REFERENCE: 00162/HG

; CURRENT APPLICATION NUMBER: US/09/508,753B

; CURRENT FILING DATE: 2000-06-16

; PRIOR APPLICATION NUMBER: JP 9/270324

; PRIOR FILING DATE: 1997-09-18

; NUMBER OF SEQ ID NOS: 472

; SEQ ID NO 65

; LENGTH: 10

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Primer

US-09-508-753B-65

## Query Match

Best Local Similarity 47.1%; Score 8; DB 1; Length 10;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TCAGCAAC 9  
|||||  
Db 1 TCAGCAAC 8

## RESULT 21

US-09-508-753B-78/c

## Query Match

Best Local Similarity 47.1%; Score 8; DB 1; Length 11;

Matches 8; Conservative 100.0%; Pred. No. 13;

; Sequence 78; Application US/09508753B  
; Patent No. 6544736  
; GENERAL INFORMATION:  
; APPLICANT: Akira SHIMAMOTO  
; APPLICANT: Yasuhiro FURUICHI  
; APPLICANT: Yuko SHIBATA  
; APPLICANT: Hiroko FUNAKI  
; APPLICANT: Eiiji OHARA  
; APPLICANT: Masanori WATAHIKI  
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample  
; FILE REFERENCE: 00162/HG  
; CURRENT APPLICATION NUMBER: US/09/508,753B  
; CURRENT FILING DATE: 2000-06-16  
; PRIOR APPLICATION NUMBER: JP 9/270324  
; PRIOR FILING DATE: 1997-09-18  
; NUMBER OF SEQ ID NOS: 472  
; SEQ ID NO 78  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Primer  
US-09-508-753B-78

## Query Match

Best Local Similarity 47.1%; Score 8; DB 1; Length 10;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCAGCAA 8  
|||||  
Db 8 CTCAGCAA 1

## RESULT 22

US-08-891-789B-11

; Sequence 11, Application US/08891789B

; Patent No. 6103466

; GENERAL INFORMATION:

; APPLICANT: Grobet, Luc; Georges, Michel

; TITLE OF INVENTION: Double-Muscling in Mammals

; NUMBER OF SEQUENCES: 52

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Blake, Cassels &amp; Graydon

; STREET: Box 25, Commerce Court West

; CITY: Toronto

; STATE: Ontario

; ZIP: M5L 1A9

; COUNTRY: Canada

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage

; COMPUTER: COMPAQ, IBM PC compatible

; OPERATING SYSTEM: MS-DOS 5.1

; SOFTWARE: WORD PERFECT

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/891,789B

; FILING DATE: July 14, 1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Hunt, John C.

; REGISTRATION NUMBER: 36,424

; REFERENCE/DOCKET NUMBER: 52836/00004

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (416) 863-4344

; TELEFAX: (416) 863-2653

; INFORMATION FOR SEQ ID NO: 11:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-891-789B-11

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 AACACTCC 14  
| | | | |  
Db 4 AACACTCC 11

## RESULT 23

US-09-990-186-59/c  
; Sequence 59, Application US/09990186  
; Patent No. 7030215  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; FILE REFERENCE: 8325-0011.21 / S11-US3  
; CURRENT APPLICATION NUMBER: US/09/990,186  
; CURRENT FILING DATE: 2001-11-20  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 59  
; LENGTH: 9  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-990-186-59

Query Match 43.5%; Score 7.4; DB 1; Length 9;  
Best Local Similarity 88.9%; Pred. No. 1.3e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTCAGCAAC 9  
| | | | |  
Db 9 CTCAGCATC 1

## RESULT 24

US-09-990-186-60/c  
; Sequence 60, Application US/09990186  
; Patent No. 7030215  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; FILE REFERENCE: 8325-0011.21 / S11-US3  
; CURRENT APPLICATION NUMBER: US/09/990,186  
; CURRENT FILING DATE: 2001-11-20  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 60  
; LENGTH: 9  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-990-186-60

Query Match 43.5%; Score 7.4; DB 1; Length 9;  
Best Local Similarity 88.9%; Pred. No. 1.3e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTCAGCAAC 9  
| | | | |  
Db 9 CTCAGCATC 1

## RESULT 25

US-09-990-186-61/c  
; Sequence 61, Application US/09990186  
; Patent No. 7030215

; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; FILE REFERENCE: 8325-0011.21 / S11-US3  
; CURRENT APPLICATION NUMBER: US/09/990,186  
; CURRENT FILING DATE: 2001-11-20  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 61  
; LENGTH: 9  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-990-186-61

Query Match 43.5%; Score 7.4; DB 1; Length 9;  
Best Local Similarity 88.9%; Pred. No. 1.3e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTCAGCAAC 9  
| | | | |  
Db 9 CTCAGCATC 1

## RESULT 26

US-09-990-186-119/c  
; Sequence 119, Application US/09990186  
; Patent No. 7030215  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; FILE REFERENCE: 8325-0011.21 / S11-US3  
; CURRENT APPLICATION NUMBER: US/09/990,186  
; CURRENT FILING DATE: 2001-11-20  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 119  
; LENGTH: 9  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-990-186-119

Query Match 43.5%; Score 7.4; DB 1; Length 9;  
Best Local Similarity 88.9%; Pred. No. 1.3e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTCAGCAAC 9  
| | | | |  
Db 9 CTCAGCATC 1

## RESULT 27

US-09-990-186-2353/c  
; Sequence 2353, Application US/09990186  
; Patent No. 7030215  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; FILE REFERENCE: 8325-0011.21 / S11-US3  
; CURRENT APPLICATION NUMBER: US/09/990,186  
; CURRENT FILING DATE: 2001-11-20  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2353  
; LENGTH: 9

```
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; US-09-990-186-2353

Query Match      43.5%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      8 ACACCTCCTA 16
      | |||||
Db      9 AACCTCCTA 1

RESULT 28
US-09-990-186-2356/c
; Sequence 2356, Application US/09990186
; Patent No. 7030215
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2356
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; US-09-990-186-2356

Query Match      43.5%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      8 ACACCTCCTA 16
      | |||||
Db      9 AACCTCCTA 1

RESULT 29
US-09-990-186-2357/c
; Sequence 2357, Application US/09990186
; Patent No. 7030215
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2357
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; US-09-990-186-2357

Query Match      43.5%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      8 ACACCTCCTA 16
      | |||||
Db      9 AACCTCCTA 1

RESULT 30
US-09-990-186-2431/c
; Sequence 2431, Application US/09990186
; Patent No. 7030215
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2431
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; US-09-990-186-2431

Query Match      43.5%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      8 ACACCTCCTA 16
      | |||||
Db      9 AACCTCCTA 1

RESULT 31
US-09-990-186-2462/c
; Sequence 2462, Application US/09990186
; Patent No. 7030215
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2462
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; US-09-990-186-2462

Query Match      43.5%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      8 ACACCTCCTA 16
      | |||||
Db      9 AACCTCCTA 1

RESULT 32
US-08-388-353-534/c
; Sequence 534, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
```

```
Qy      8 ACACCTCCTA 16
      | |||||
Db      9 AACCTCCTA 1

RESULT 30
US-09-990-186-2431/c
; Sequence 2431, Application US/09990186
; Patent No. 7030215
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2431
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; US-09-990-186-2431

Query Match      43.5%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      8 ACACCTCCTA 16
      | |||||
Db      9 AACCTCCTA 1

RESULT 31
US-09-990-186-2462/c
; Sequence 2462, Application US/09990186
; Patent No. 7030215
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2462
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; US-09-990-186-2462

Query Match      43.5%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      8 ACACCTCCTA 16
      | |||||
Db      9 AACCTCCTA 1

RESULT 32
US-08-388-353-534/c
; Sequence 534, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
```

```
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/388,353
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 534:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-388-353-534

Query Match 43.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 19;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 AACACTCCT 15
Db 10 AACACTTCT 2
||||| |||

RESULT 33
US-08-388-353-535/c
; Sequence 535, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
```

```
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 535:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-388-353-535

Query Match 43.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 19;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 AACACTCCT 15
Db 9 AACACTTCT 1
||||| |||

RESULT 34
US-08-488-551B-534/c
; Sequence 534, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PNO284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 534:
; SEQUENCE CHARACTERISTICS:
```

LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-488-551B-534

Query Match 43.5%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 19;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 AACACTCT 15  
Db 10 AACACTTCT 2

RESULT 35  
US-08-488-551B-535/c  
Sequence 535, Application US/08488551B  
Patent No. 6015661  
GENERAL INFORMATION:  
APPLICANT: Nicholas J. Deacon  
APPLICANT: Dale A. McPhee  
APPLICANT: David Cooper  
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1  
NUMBER OF SEQUENCES: 841  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER  
STREET: 400 GARDEN CITY PLAZA  
CITY: GARDEN CITY  
STATE: NEW YORK  
COUNTRY: U.S.A.  
ZIP: 11530-0299  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION NUMBER: US/08/488,551B  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PM3864 (AU)  
FILING DATE: 14-FEB-1994  
APPLICATION NUMBER: PM4002 (AU)  
FILING DATE: 21-FEB-1994  
APPLICATION NUMBER: PM0284 (AU)  
FILING DATE: 23-DEC-1994  
APPLICATION NUMBER: US 08/388,353  
FILING DATE: 14-FEB-1995  
APPLICATION NUMBER: PM3021/95  
FILING DATE: 17-MAY-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: FRANK S. DIGILIO  
REFERENCE/DOCKET NUMBER: 9606Z  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (516) 742-4343  
TELEFAX: (516) 742-4366  
INFORMATION FOR SEQ ID NO: 535:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-488-551B-535

Query Match 43.5%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 19;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 AACACTCT 15  
Db 10 AACACTTCT 2

Db 9 AACACTTCT 1

RESULT 36  
US-08-088-661F-37/c  
Sequence 37, Application US/08088661F  
Patent No. 6228982  
GENERAL INFORMATION:  
APPLICANT: No. 6228982den, Bengel  
APPLICANT: Wittung, Pernilla  
APPLICANT: Buchardt, Ole  
APPLICANT: Egholm, Michael  
APPLICANT: Nielsen, Peter E.  
APPLICANT: Berg, Rolf  
TITLE OF INVENTION: Double-Stranded Peptide Nucleic Acids  
FILE REFERENCE: ISIS1108  
CURRENT APPLICATION NUMBER: US/08/088,661F  
CURRENT FILING DATE: 1993-07-02  
PRIOR APPLICATION NUMBER: 08/054,363  
PRIOR FILING DATE: 1993-04-26  
PRIOR APPLICATION NUMBER: PCT/EP92/01219  
PRIOR FILING DATE: 1992-05-19  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 37  
LENGTH: 10  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: No. 6228982el Sequence  
US-08-088-661F-37

Query Match 43.5%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 19;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CACTCTAT 17  
Db 10 CACTACTAT 2

RESULT 37  
US-09-173-936B-1/c  
Sequence 1, Application US/09173936B  
Patent No. 6238865  
GENERAL INFORMATION:  
APPLICANT: Zhen, Huang; Sostak, Jack W.  
TITLE OF INVENTION: A Simple and Efficient Method to Label and Modify 3'-Terminal  
of RNA Using DNA Polymerase and a Synthetic Template with D Nucleotides  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cohen, Pontani, Lieberman & Pavane  
STREET: 551 Fifth Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10176  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.50 inch Diskette  
COMPUTER: IBM-MS  
OPERATING SYSTEM: Window 95  
SOFTWARE: Microsoft Word  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/173,936B  
FILING DATE: 16-Oct-1998  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/063,757  
FILING DATE: 17-OCT-1997  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:

; LENGTH: 10 bases  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-173-936B-1

Query Match 43.5%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 19;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CAGCAACAC 11  
Db 9 CAGCAACCC 1

RESULT 38  
US-08-108-591B-35/c  
; Sequence 35, Application US/08108591B  
; Patent No. 6395474  
; GENERAL INFORMATION:  
; APPLICANT: Buchardt, Ole  
; APPLICANT: Egholm, Michael  
; APPLICANT: Nielsen, Peter Bigil  
; APPLICANT: Berg, Rolf Henrik  
; TITLE OF INVENTION: Peptide Nucleic Acids  
; FILE REFERENCE: ISIS0540  
; CURRENT APPLICATION NUMBER: US/08/108,591B  
; CURRENT FILING DATE: 2001-08-13  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 35  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: No. 6395474el Sequence  
US-08-108-591B-35

Query Match 43.5%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 19;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CACTCTAT 17  
Db 10 CACTACTAT 2

RESULT 39  
US-09-632-538C-7/c  
; Sequence 7, Application US/09632538C  
; Patent No. 6440674  
; GENERAL INFORMATION:  
; APPLICANT: Misra, Santosh et al.  
; TITLE OF INVENTION: PLANT PROMOTER DERIVED FROM LUMINAL BINDING PROTEIN GENE AND METH  
; FILE REFERENCE: 54359  
; CURRENT APPLICATION NUMBER: US/09/632,538C  
; CURRENT FILING DATE: 2000-08-04  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: PROMOTER  
; OTHER INFORMATION: ELEMENT  
US-09-632-538C-7

Query Match 43.5%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 19;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CAGCAACAC 11  
Db 9 CAGCAACCC 1

US-08-479-660-16  
; Sequence 16, Application US/08479660  
; Patent No. 6475806  
; GENERAL INFORMATION:  
; APPLICANT: Benjamin, Howard  
; APPLICANT: Signer, Ethan  
; APPLICANT: Geiter, Malcolm  
; TITLE OF INVENTION: ANCHOR LIBRARIES AND IDENTIFICATION  
; TITLE OF INVENTION: OF PEPTIDE BINDING SEQUENCES  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
; STREET: 600 Atlantic Avenue  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA: US/08/479,660  
; APPLICATION NUMBER: US/08/479,660  
; FILING DATE:  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Greer, Helen  
; REGISTRATION NUMBER: 36,816  
; REFERENCE/DOCKET NUMBER: P0567/7000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 720-3500  
; TELEFAX: (617) 720-2441  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-479-660-16

Query Match 43.5%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 19;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CAGCAACAC 11  
Db 1 CAGCAACAC 9

Query Match 43.5%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 19;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

US-09-627-536-7/c  
; Sequence 7, Application US/09627536  
; Patent No. 6541222  
; GENERAL INFORMATION:  
; APPLICANT: Misra, Santosh et al.,  
; TITLE OF INVENTION: PLANT GENE PROMOTER ISOLATED FROM DOUGLAS-FIR 2S SEED STORAGE PR  
; FILE REFERENCE: 54094  
; CURRENT APPLICATION NUMBER: US/09/627,536  
; CURRENT FILING DATE: 2000-07-28  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 10  
; TYPE: DNA

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; ORGANISM: Pseudotsuga menziesii
US-09-627-536-7

Query Match      43.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 19;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 CTCAGCAAC 9
Db      9 CTCACCAAC 1

RESULT 42
US-08-894-454-120/c
; Sequence 120, Application US/08894454
; Patent No. 6544784
; GENERAL INFORMATION:
; APPLICANT: VAN DEN VEN, W.J.M.
; APPLICANT: SCHOENMAKERS, H.F.P.M.
; TITLE OF INVENTION: MULTIPLE-TUMOR ABERRENT GROWTH
; TITLE OF INVENTION: GENES
; NUMBER OF SEQUENCES: 164
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Webb Law Firm
; STREET: 700 Koppers Building, 436 Seventh Avenue
; CITY: Pittsburgh
; STATE: PA
; COUNTRY: USA
; ZIP: 15219-1818
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/894,454
; FILING DATE: 15-AUG-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP/00716
; FILING DATE: 19-FEB-1996
; APPLICATION NUMBER: 95200390.3
; FILING DATE: 17-FEB-1995
; APPLICATION NUMBER: 95201951.1
; FILING DATE: 14-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Johnson, Barbara E
; REGISTRATION NUMBER: 31,198
; REFERENCE/DOCKET NUMBER: 702-971100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 412-471-8815
; TELEFAX: 412-471-4094
; TELEX:
; INFORMATION FOR SEQ ID NO: 120:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-894-454-120

Query Match      43.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 19;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      7 AACACTCCT 15
Db      10 AAAACTCCT 2

RESULT 43
US-09-525-906-10
; Sequence 10, Application US/09525906
```

```
; Patent No. 6605433
; GENERAL INFORMATION:
; APPLICANT: Jen, Jen
; APPLICANT: Sidransky, David
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; APPLICANT: Fliss, Makiko
; APPLICANT: Polyak, Kornelia
; TITLE OF INVENTION: Mitochondrial Dosimeter
; FILE REFERENCE: 1107.85815
; CURRENT APPLICATION NUMBER: US/09/525,906
; CURRENT FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 09/377,856
; PRIOR FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: 60/097,307
; PRIOR FILING DATE: 1998-08-20
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-525-906-10

Query Match      43.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 19;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      8 ACACTCCTA 16
Db      2 ACACTACTA 10

RESULT 44
US-08-468-719A-35/c
; Sequence 35, Application US/08468719A
; Patent No. 6710163
; GENERAL INFORMATION:
; APPLICANT: Buchardt, Ole
; APPLICANT: Egholm, Michael
; APPLICANT: Nielsen, Peter E.
; APPLICANT: Berg, Rolf H.
; TITLE OF INVENTION: PEPTIDE NUCLEIC ACIDS SYNTHONS
; FILE REFERENCE: ISPS-1999
; CURRENT APPLICATION NUMBER: US/08/468,719A
; CURRENT FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/108,591
; PRIOR FILING DATE: 1993-11-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide Primer
US-08-468-719A-35

Query Match      43.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 19;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      9 CACTCCTAT 17
Db      10 CACTACTAT 2

RESULT 45
US-08-462-977B-35/c
; Sequence 35, Application US/08462977B
; Patent No. 6713602
; GENERAL INFORMATION:
; APPLICANT: Buchardt, Ole
```

; APPLICANT: Egholm, Michael  
; APPLICANT: Nielsen, Peter Bigil  
; APPLICANT: Berg, Rolf Henrik  
; TITLE OF INVENTION: Peptide Nucleic Acids  
; FILE REFERENCE: ISIS-1993  
; CURRENT APPLICATION NUMBER: US/08/462,977B  
; CURRENT FILING DATE: 1995-06-05  
; PRIOR APPLICATION NUMBER: 1995-06-05  
; PRIOR FILING DATE: 1993-11-22  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 35  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: No. 6713602el Sequence  
US-08-462-977B-35

Query Match 43.5%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 19;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CACTCTCTAT 17  
|||||  
Db 10 CACTACTAT 2

RESULT 46  
US-09-641-540-7/c  
; Sequence 7, Application US/09641540  
; Patent No. 6759529  
; GENERAL INFORMATION:  
; APPLICANT: Miera, Santosh  
; TITLE OF INVENTION: PLANT-GENE PROMOTER AND METHODS OF USING THE SAME  
; FILE REFERENCE: 54358  
; CURRENT APPLICATION NUMBER: US/09/641,540  
; CURRENT FILING DATE: 2000-08-18  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: PROMOTER  
; OTHER INFORMATION: ELEMENT  
US-09-641-540-7

Query Match 43.5%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 19;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTCAGCAAC 9  
|||||  
Db 9 CTCACCAAC 1

RESULT 47  
US-09-748-710-24/c  
; Sequence 24, Application US/09748710  
; Patent No. 6916610  
; GENERAL INFORMATION:  
; APPLICANT: WANG, SAN MING  
; APPLICANT: CHEN, JIANJUN  
; APPLICANT: ROWLEY, JANET D.  
; TITLE OF INVENTION: METHOD FOR GENERATION OF LONGER CDNA FRAGMENTS  
; FILE REFERENCE: ARCD:343US  
; CURRENT APPLICATION NUMBER: US/09/748,710  
; CURRENT FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/174,391

; PRIOR FILING DATE: 2000-01-03  
; PRIOR APPLICATION NUMBER: 60/173,617  
; PRIOR FILING DATE: 1999-12-29  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 24  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Primer  
US-09-748-710-24

Query Match 43.5%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 19;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TCAGCAACA 10  
|||||  
Db 10 TCACCAACA 2

RESULT 48  
PCT-US96-09383-16  
; Sequence 16, Application PC/TUS9609383  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: ANCHOR LIBRARIES AND IDENTIFICATION  
; TITLE OF INVENTION: PEPTIDE BINDING SEQUENCES  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
; STREET: 600 Atlantic Avenue  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/09383  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/479,660  
; FILING DATE: 07-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Greer, Helen  
; REGISTRATION NUMBER: 36,816  
; REFERENCE/DOCKET NUMBER: P0567/7000WO  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 720-3500  
; TELEFAX: (617) 720-2441  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
PCT-US96-09383-16

Query Match 43.5%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 19;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CAGCAACAC 11  
|||||  
Db 1 CAGCACCAC 9



RESULT 49  
US-08-859-954-7/C  
; Sequence 7, Application US/08859954  
; Patent No. 6083695  
; GENERAL INFORMATION:  
; APPLICANT: Hardin, Susan H.  
; APPLICANT: Homayouni, Ramin  
; APPLICANT: Hardin, Paul E.  
; TITLE OF INVENTION: Design and Optimized Primer Library for  
; NUMBER OF SEQUENCES: 566  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fulbright & Jaworski L.L.P.  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: U.S.A.  
; ZIP: 77010-3095  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/859,954  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/632,782  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Paul, Thomas D.  
; REGISTRATION NUMBER: 32,714  
; REFERENCE/DOCKET NUMBER: D-5900  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 713/651-5325  
; TELEFAX: 713/651-5246  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "oligonucleotide"  
; HYPOTHETICAL: YES  
; ANTI-SENSE: YES  
US-08-859-954-7  
Query Match 41.2%; Score 7; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 TCAGCAA 8  
DB 7 TCAGCAA 1  
RESULT 50  
US-08-859-954-314  
; Sequence 314, Application US/08859954  
; Patent No. 6083695  
; GENERAL INFORMATION:  
; APPLICANT: Hardin, Susan H.  
; APPLICANT: Homayouni, Ramin  
; APPLICANT: Hardin, Paul E.  
; TITLE OF INVENTION: Design and Optimized Primer Library for  
; NUMBER OF SEQUENCES: 566  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fulbright & Jaworski L.L.P.  
; STREET: 1301 McKinney, Suite 5100

CITY: Houston  
STATE: Texas  
COUNTRY: U.S.A.  
ZIP: 77010-3095  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/859,954  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/632,782  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Paul, Thomas D.  
REGISTRATION NUMBER: 32,714  
REFERENCE/DOCKET NUMBER: D-5900  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 713/651-5325  
TELEFAX: 713/651-5246  
INFORMATION FOR SEQ ID NO: 314:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "oligonucleotide"  
HYPOTHETICAL: YES  
ANTI-SENSE: YES  
US-08-859-954-314  
Query Match 41.2%; Score 7; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CTCAGCA 7  
DB 1 CTCAGCA 7  
RESULT 51  
US-08-859-954-335/C  
; Sequence 335, Application US/08859954  
; Patent No. 6083695  
; GENERAL INFORMATION:  
; APPLICANT: Hardin, Susan H.  
; APPLICANT: Homayouni, Ramin  
; APPLICANT: Hardin, Paul E.  
; TITLE OF INVENTION: Design and Optimized Primer Library for  
; NUMBER OF SEQUENCES: 566  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fulbright & Jaworski L.L.P.  
; STREET: 1301 McKinney, Suite 5100  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: U.S.A.  
; ZIP: 77010-3095  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/859,954  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/632,782

```
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, Thomas D.
; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5900
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/651-5325
; TELEFAX: 713/651-5246
; INFORMATION FOR SEQ ID NO: 335:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "oligonucleotide"
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
; US-08-859-954-335

Query Match 41.2%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 ACATCC 14
Db 8 ACATCC 2

RESULT 52
US-08-859-954-452/c
; Sequence 452, Application US/08859954
; Patent No. 6083695
; GENERAL INFORMATION:
; APPLICANT: Hardin, Susan H.
; APPLICANT: Homayouni, Ramin
; APPLICANT: Hardin, Paul E.
; TITLE OF INVENTION: Design and Optimized Primer Library for
; TITLE OF INVENTION: Gene Sequencing and Method Thereof
; NUMBER OF SEQUENCES: 566
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,954
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/632,782
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, Thomas D.
; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5900
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/651-5325
; TELEFAX: 713/651-5246
; INFORMATION FOR SEQ ID NO: 452:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid

; DESCRIPTION: /desc = "oligonucleotide"
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
; US-08-859-954-452

Query Match 41.2%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CACTCCT 15
Db 7 CACTCCT 1

RESULT 53
US-09-990-186-453/c
; Sequence 453, Application US/09990186
; Patent No. 7030215
; GENERAL INFORMATION:
; APPLICANT: Liu, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 453
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
; US-09-990-186-453

Query Match 41.2%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CAGCAAC 9
Db 7 CAGCAAC 1

RESULT 54
US-09-990-186-454/c
; Sequence 454, Application US/09990186
; Patent No. 7030215
; GENERAL INFORMATION:
; APPLICANT: Liu, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 454
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
; US-09-990-186-454

Query Match 41.2%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CAGCAAC 9
Db 7 CAGCAAC 1
```

```
Db          7 CAGCAAC 1

RESULT 55
US-09-593-323-55/c
; Sequence 55, Application US/09593323
; Patent No. 6265213
; GENERAL INFORMATION:
; APPLICANT: Morgan, Antony R.
; APPLICANT: Severini, Alberto
; TITLE OF INVENTION: Compositions and Methods for Determining the Activity
; TITLE OF INVENTION: of DNA-Binding Proteins and of Initiation of
; FILE REFERENCE: DNAB-02921
; CURRENT APPLICATION NUMBER: US/09/593,323
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: 09/344,300
; PRIOR FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-593-323-55

Query Match          41.2%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 CTCAGCA 7
Db          7 CTCAGCA 1

RESULT 56
US-09-594-108-55/c
; Sequence 55, Application US/09594108
; Patent No. 6284468
; GENERAL INFORMATION:
; APPLICANT: Morgan, Antony R.
; APPLICANT: Severini, Alberto
; TITLE OF INVENTION: Compositions and Methods for Determining the Activity
; TITLE OF INVENTION: of DNA-Binding Proteins and of Initiation of
; FILE REFERENCE: DNAB-02921
; CURRENT APPLICATION NUMBER: US/09/594,108
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: 09/344,300
; PRIOR FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-594-108-55

Query Match          41.2%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 CTCAGCA 7
Db          7 CTCAGCA 1

RESULT 57
US-09-344-300-55/c
; Sequence 55, Application US/09344300B
; Patent No. 6297013
; GENERAL INFORMATION:
; APPLICANT: Morgan, Antony R.
; APPLICANT: Severini, Alberto
; TITLE OF INVENTION: Compositions and Methods for Determining the Activity
; TITLE OF INVENTION: of DNA-Binding Proteins and of Initiation of
; FILE REFERENCE: DNAB-02921
; CURRENT APPLICATION NUMBER: US/09/344,300B
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-344-300-55

Query Match          41.2%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 CTCAGCA 7
Db          7 CTCAGCA 1

RESULT 58
US-09-101-272G-91/c
; Sequence 91, Application US/09101272G
; Patent No. 6509445
; GENERAL INFORMATION:
; APPLICANT: Nissin Food Products Co., Ltd.
; TITLE OF INVENTION: CANCEROUS METASTASIS INHIBITOR
; FILE REFERENCE: Q50979
; CURRENT APPLICATION NUMBER: US/09/101,272G
; CURRENT FILING DATE: 1998-07-08
; PRIOR APPLICATION NUMBER: JP 1059/1996
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 91
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: 5' end of HI-8 UTI DNA fragment (coding strand)
US-09-101-272G-91

Query Match          41.2%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          3 CAGCAAC 9
Db          8 CAGCAAC 2

RESULT 59
US-09-508-753B-61/c
; Sequence 61, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Eiichi OHARA
; APPLICANT: Masanori WATAHIKI
```

; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample  
; FILE REFERENCE: 00162/HG  
; CURRENT APPLICATION NUMBER: US/09/508,753B  
; CURRENT FILING DATE: 2000-06-16  
; PRIOR APPLICATION NUMBER: JP 9/270324  
; PRIOR FILING DATE: 1997-09-18  
; NUMBER OF SEQ ID NOS: 472  
; SEQ ID NO 61  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Primer  
US-09-508-753B-61

Query Match 41.2%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCAGCA 7  
| | | | |  
Db 10 CTCAGCA 4

RESULT 60  
US-09-508-753B-159  
; Sequence 159, Application US/09508753B  
; Patent No. 6544736  
; GENERAL INFORMATION:  
; APPLICANT: Akira SHIMAMOTO  
; APPLICANT: Yasuhiro FURUICHI  
; APPLICANT: Yuko SHIBATA  
; APPLICANT: Hiroko FUNAKI  
; APPLICANT: Eiji OHARA  
; APPLICANT: Masanori WATAHIKI  
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample  
; FILE REFERENCE: 00162/HG  
; CURRENT APPLICATION NUMBER: US/09/508,753B  
; CURRENT FILING DATE: 2000-06-16  
; PRIOR APPLICATION NUMBER: JP 9/270324  
; PRIOR FILING DATE: 1997-09-18  
; NUMBER OF SEQ ID NOS: 472  
; SEQ ID NO 159  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Primer  
US-09-508-753B-159

Query Match 41.2%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCAGCA 7  
| | | | |  
Db 1 CTCAGCA 7

RESULT 61  
US-09-825-770-1/c  
; Sequence 1, Application US/09825770  
; Patent No. 6686180  
; GENERAL INFORMATION:  
; APPLICANT: Blake, Milan S.  
; APPLICANT: Bogdan, John A.  
; APPLICANT: Nazario-Larrieu, Javier  
; TITLE OF INVENTION: Improved Method for the Production of  
; TITLE OF INVENTION: Bordatella Pertussis Toxin  
; FILE REFERENCE: NV1933  
; CURRENT APPLICATION NUMBER: US/09/825,770  
; CURRENT FILING DATE: 2001-04-04  
; PRIOR APPLICATION NUMBER: 60/194,482

; PRIOR FILING DATE: 2000-04-04  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: recombinant DNA  
US-09-825-770-1

Query Match 41.2%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TCAGCAA 8  
| | | | |  
Db 9 TCAGCAA 3

RESULT 62  
US-10-677-496-1/c  
; Sequence 1, Application US/10677496  
; Patent No. 7018813  
; GENERAL INFORMATION:  
; APPLICANT: Blake, Milan S.  
; APPLICANT: Bogdan, John A.  
; APPLICANT: Nazario-Larrieu, Javier  
; TITLE OF INVENTION: Improved Method for the Production of  
; TITLE OF INVENTION: Bordatella Pertussis Toxin  
; FILE REFERENCE: NV1933  
; CURRENT APPLICATION NUMBER: US/10/677,496  
; CURRENT FILING DATE: 2003-10-03  
; PRIOR APPLICATION NUMBER: US/09/825,770  
; PRIOR FILING DATE: 2001-04-04  
; PRIOR APPLICATION NUMBER: 60/194,482  
; PRIOR FILING DATE: 2000-04-04  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: recombinant DNA  
US-10-677-496-1

Query Match 41.2%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TCAGCAA 8  
| | | | |  
Db 9 TCAGCAA 3

RESULT 63  
US-09-263-790-23  
; Sequence 23, Application US/09263790  
; Patent No. PPI2997  
; GENERAL INFORMATION:  
; APPLICANT: Nirmal Kumar PATRA et al.  
; TITLE OF INVENTION: JAL PALLAVI, WATER LOGGING TOLERANT CYMBOPOGON WINTERIANUS  
; FILE REFERENCE: 2761-0120P  
; CURRENT APPLICATION NUMBER: US/09/263,790  
; CURRENT FILING DATE: 1999-03-05  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 23  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:

Tue Nov 21 14:35:55 2006

; OTHER INFORMATION: OPT 03 Primer - Used to develop the unique RAPD profiles of the  
; OTHER INFORMATION: plant Jal Pallavi  
US-09-263-790-23

Query Match 41.2%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CACTCCT 15  
| | | | |  
Db 3 CACTCCT 9 .

RESULT 64

US-09-721-777-3

; Sequence 3, Application US/09721777

; Patent No. PP13279

; GENERAL INFORMATION:

; APPLICANT: Khanuja, Suman Preet Singh

; APPLICANT: Kumar, Sushil

; APPLICANT: Shasany, Ajit Kumar

; APPLICANT: Dhawan, Sunita

; APPLICANT: Darokar, Mahendra Pandurang

; APPLICANT: Naqvi, Ali Arif

; APPLICANT: Dhawan, Om Parkash

; APPLICANT: Singh, Anil Kumar

; APPLICANT: Patra, Nirmal Kumar

; APPLICANT: Bahl, Janak Raj

; APPLICANT: Bansal, Ram Prakash

; TITLE OF INVENTION: Mint Plant Named Saksham

; FILE REFERENCE: 033166-002

; CURRENT APPLICATION NUMBER: US/09/721,777

; CURRENT FILING DATE: 2000-11-27

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 10

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: OPT primer

US-09-721-777-3

Query Match 41.2%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CACTCCT 15  
| | | | |  
Db 3 CACTCCT 9

Search completed: November 21, 2006, 14:30:59

Job time : 0.001 secs

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